

Please amend the application as follows.

IN THE SPECIFICATION:

Please amend the specification in accordance with § 1.52(e)(5) and § 1.77(b)(4) at page 1, line 35 following the Statement Regarding Federally Sponsored Research or Development to include the following paragraph:

BC *Sette*
--The Sequence Listing written in file 141ultra.txt, 2,439,302 bytes, created on November 15, 2000 on two identical copies of compact discs for Application No: 09/412,863, Sette et al., Inducing Cellular Immune Responses To Human Immunodeficiency Virus-1 Using Peptide And Nucleic Acid Compositions, is hereby incorporated by reference.--

Please delete each page of Tables IV, V, IX, XX, XXIII, XXIV, XXVII-XXXIII, and XXXV-XXXIX and insert therefor each page of the replacement Tables IV, V, IX, XX, XXIII, XXIV, XXVII, XXXIII, and XXXV-XXXIX submitted herewith.

On page 52, line 3, after 'QYIKANSKFIGITE', please insert --; SEQ ID NO:14488--.

On page 52 line 4, after 'DIEKKIAKMEKASSVFNVNS', please insert --; SEQ ID NO:14489--.

On page 52 line 5, after 'GAVDSILGGVATYGAA', please insert --; SEQ ID NO:14490--.

On page 52, line 12, after 'aKXVWANTLKAAa', please insert --(SEQ ID NO: 14491)--.

The amendment to the specification adds no new matter. The amendment sets out the SEQ ID NOs. for sequences present in the application as filed.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Jean M. Lockyer
Jean M. Lockyer
Reg. No. 44,879



RECEIVED

DEC 04 2000

TECH CENTER 1600/2900

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQ ID	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	14492	YLEPAIAKY	25
A*0201	941.01	14493	FLPSDYFPSV	5.0
A*0202	941.01	14494	FLPSDYFPSV	4.3
A*0203	941.01	14495	FLPSDYFPSV	10
A*0205	941.01	14496	FLPSDYFPSV	4.3
A*0206	941.01	14497	FLPSDYFPSV	3.7
A*0207	941.01	14498	FLPSDYFPSV	23
A*6802	1141.02	14499	FTQAGYPAL	40
A*0301	941.12	14500	KVFPYALINK	11
A*1101	940.06	14501	AVDLYHFLK	6.0
A*3101	941.12	14502	KVFPYALINK	18
A*3301	1083.02	14503	STLPETYVRR	29
A*6801	941.12	14504	KVFPYALINK	8.0
A*2402	979.02	14505	AYIDNYNKF	12
B*0702	1075.23	14506	APRTLVL	5.5
B*3501	1021.05	14507	FPFKYAAAF	7.2
B51	1021.05	14508	FPFKYAAAF	5.5
B*5301	1021.05	14509	FPFKYAAAF	9.3
B*5401	1021.05	14510	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	SEQ ID	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	14511	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	14512	YKTIAFDDEEARR	300
DRB1*0401	DR4w4	515.01	14513	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	14514	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	14515	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	14516	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	14517	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	14518	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	14519	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	14520	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	14521	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	14522	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	14523	GRTQDENPVVHFFK NIVTPRTPPP	9.1
DRB3*0101	DR52a	511	14524	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	14525	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	14526	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table XIXa

HIV DR Super Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	VSTQLLNG	13520	61	95	KPVVSTQLLLNGSLA	12864	299	29	45
ENV	VSTQLLLN	13521	60	94	IKPVVSTQLLLNGSL	12865	298	29	45
ENV	LTWVGKQL	13522	59	92	LLQLTVWGIKQLQAR	12866	651	26	41
ENV	LLSGIVQQ	13523	58	91	ARQLSGIVQQSNL	12867	627	22	34
ENV	WATHACVPT	13524	56	88	HNWATHACVPTDPN	12868	79	44	69
ENV	LGAAGSTMG	13525	55	86	LGFLGAAGSTMGAAS	12869	605	36	56
ENV	VRQYSPLS	13526	55	86	VNRVRQYSPLSFQT	12870	800	36	57
ENV	LLNGSLAE	13527	54	84	STQLLLNGSLAEFV	12871	303	16	25
ENV	VKLTPLCVT	13528	53	83	KPCVKLTPLCVTLNC	12872	130	29	45
ENV	LRAEAQHH	13529	51	80	NNLLRAIEAQHHLLQ	12873	639	18	28
ENV	VSTVQCTHIG	13530	51	80	CKNVSTVQCTHIGKP	12874	285	14	22
ENV	LGIWGCSSGK	13531	50	78	QQLLGIWGCSSGKLC	12875	676	46	72
ENV	LWDQSLKPC	13532	50	78	IISLWDQSLKPCVKL	12876	121	35	55
ENV	LGFLGAAGS	13533	49	77	AVFLGFLGAAGSTMG	12877	602	19	30
ENV	VWATHACVP	13534	49	77	VHNWATHACVPTDP	12878	78	34	53
ENV	WGKIQAR	13535	49	77	LTWVGKIQARVLA	12879	654	39	61
ENV	LWYKIFIM	13536	43	67	TNWLWYKIFIMIVG	12880	771	11	17
ENV	FCASDAKAY	13537	42	66	TTLFCASDAKAYDTE	12881	61	18	28
ENV	IVGGLIGLR	13538	42	66	FIMIVGGLIGLRIVF	12882	780	22	34
ENV	IFIMIVGGL	13539	41	64	YKIFIMIVGGLIGL	12883	776	22	34
ENV	VYGVVPVWK	13540	41	64	WVTVYGVVPVWKEAT	12884	46	22	34
ENV	IKQLQARVL	13541	40	63	VWGIKQLQARVLAVE	12885	656	31	49
ENV	IKIFIMIVG	13542	39	61	LWYKIFIMIVGGLI	12886	774	31	48
ENV	MGAASITLT	13543	39	61	GSTMGAASITLTVOA	12887	613	28	44
ENV	YKIFIMIV	13544	39	61	WLWYKIFIMIVGGL	12888	773	38	59
ENV	ITGLLLTRD	13545	37	58	SSNITGLLLTRDGGK	12889	516	06	9
ENV	IPHYCAPA	13546	36	56	FEPIPHYCAPAGFA	12890	255	21	33
ENV	MIVGGLIGL	13547	36	56	IFIMIVGGLIGLRIV	12891	779	22	34
ENV	VQARQLLSG	13548	36	56	TLTVQARQLLSGIVQ	12892	622	35	55
ENV	FEPIPHYC	13549	35	55	KVSEPIPHYCAPA	12893	854	28	44
ENV	LRSLCLFSY	13550	35	55	WDDLRLSLCLFSYHRL	12894	105	11	17
ENV	MWKNMVEQ	13551	35	55	NFNWKNMVEQMHHE	12895	75	17	27
ENV	VIINWATHA	13552	35	55	DTEVHNWATHACVP	12896	106	20	31
ENV	WKNMVEQM	13553	35	55	FNMWKNMVEQMHED	12897	47	22	34
ENV	YYGVVPVKE	13554	35	55	VTVYGVVPVWKEATT	12898	648	34	53
ENV	LLQLTVWGI	13555	34	53	QQHLLQLTVWGIKQL	12899	566	12	19
ENV	IEPLGVAPT	13556	33	52	VVKIEPLGVAPTAK	12900	295	32	50
ENV	IKPVVSTQL	13557	33	52	THGKIPVSTQLLLN	12901	659	32	50
ENV	LQARVLAVE	13558	33	52	IKQLQARVLAVERYL	12902	851	18	28
ENV	WDDLRLSL	13559	33	52	ALAWDDLRLSLCLFSY	12903	581	01	2
ENV	INIHTPHR	13560	01	50	SRPIINIHTPHREKR	12904	582	01	2
ENV	INIHTPHRE	13561	01	50	RPIINIHTPHREKR	12905	242	08	13
ENV	ITQACPKVS	13562	32	50	TSVITQACPKVSFEP	12906	631	26	41
ENV	IVQQSNLL	13563	32	50	LSGIVQQSNLLRAI	12907	151	01	2
ENV	LGNNSTNST	13564	01	50	NKTLGNNSTNSTLGN	12908	580	01	2
ENV	VISTRTHRE	13565	01	50	ARPVISTRTHREKR	12909	12	03	5
ENV	WRWGTLLFG	13566	01	50	QNLWRWGTLLFGMLM	12910	791	14	22
ENV	WRWGTMLLG	13567	01	50	QHLWRWGTMLLGMLM	12911	304	14	22
ENV	FAVLSIVNR	13568	31	48	RIVFAVLSIVNRVQ	12912			
ENV	LLNGSLAE	13569	31	48	TQLLLNGSLAEFV	12913			

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	LTPLCVTLN	13570	29	45	CVKLTPLCVTLNCTD	12914	132	11	17
ENV	LYKYKVVKI	13571	29	45	RSELYKYKVVKIEPL	12915	558	23	36
ENV	VPWNSSWSN	13572	29	45	TTNVPWNSSWSNKS	12916	691	03	5
ENV	YRLNCNTS	13573	28	44	YKEYRLNCNTSAIT	12917	232	01	8
ENV	IHYCAPAGF	13574	27	42	PIPIHYCAPAGFAIL	12918	258	26	41
ENV	LKDQQLGI	13575	27	42	ERYLKDQQLGIWGC	12919	670	25	39
ENV	YKYKVVKIE	13576	27	42	SELYKYKVVKIEPLG	12920	559	24	38
ENV	IRPVVSTQL	13577	26	41	THGIRPVVSTQLLN	12921	295	26	41
ENV	LDKWASLWN	13578	26	41	LLALDKWASLWNWFD	12922	755	08	13
ENV	LRIVFAVLS	13579	26	41	LIGLRIVFAVLSVN	12923	787	10	16
ENV	LNGSLAEIE	13580	25	39	QLLNGSLAEIEVVI	12924	305	13	20
ENV	YKVVVKIEPL	13581	25	39	LYKYKVVKIEPLGVA	12925	561	23	36
ENV	LKGLRLGWE	13582	11	37	RSSLKGLRLGWEGLK	12926	885	04	7
ENV	FSYHRLRDL	13583	23	36	LCLFSYHRLRDLILI	12927	860	08	13
ENV	INCTRPNN	13584	23	36	SVEINCTRPNNTRK	12928	340	05	8
ENV	VVKIEPLGV	13585	23	36	KYKVVVKIEPLGVAPT	12929	563	23	36
ENV	WKEATTLF	13586	23	36	VPVWKEATTLFCAS	12930	53	22	34
ENV	IGLRIVFAV	13587	22	34	GGIGLRIVFAVLSI	12931	785	12	19
ENV	FFYCNTSGL	13588	21	33	GGEFFYCNTSGLFNS	12932	441	07	11
ENV	FGLGALFLG	13589	01	33	RAAFGLGALFLGFLG	12933	594	01	2
ENV	FYCNTSGLF	13590	21	33	GEFFYCNTSGLFNST	12934	442	07	11
ENV	LIGLRIVFA	13591	21	33	VGGLIGLRIVFAVLS	12935	784	17	27
ENV	VGLGAVFLG	13592	01	33	KRAVGLGAVFLGFLG	12936	593	06	9
ENV	ICTTAVPWN	13593	20	31	KRAVGLGMLFLGVL	12937	594	01	2
ENV	ICTTNPWN	13595	20	31	GKLICTTNPWNSSW	12938	686	09	14
ENV	LGVAPTKAK	13596	19	30	IEPLGVAPTAKRRV	12940	569	15	23
ENV	LICTTAVPW	13597	19	30	SGKLICTTAVPWNS	12941	685	09	14
ENV	LRDQQLGI	13598	19	30	ERYLRDQQLGIWGC	12942	670	17	27
ENV	VFLGFLGAA	13599	19	30	LGAVFLGFLGAGST	12943	600	09	14
ENV	FSYHRLRDF	13600	18	28	LCLFSYHRLRDFILI	12944	860	08	13
ENV	IPHYCTPA	13601	18	28	FEPIPHYCTPAGFA	12945	255	10	16
ENV	IVFAVLSIV	13602	18	28	GLRIVFAVLSIVNRV	12946	789	16	25
ENV	VFAVLSIVN	13603	18	28	LRIVFAVLSIVNRV	12947	790	16	25
ENV	VPWNASWSN	13604	18	28	TTAVPWNASWSNKS	12948	691	06	9
ENV	IGLRIVFAV	13605	17	27	GGIGLRIVFAVLSI	12949	785	11	17
ENV	IRQAHCNIS	13606	17	27	IGDIRQAHCNISRAK	12950	378	02	3
ENV	VAPTAKARR	13607	17	27	PLGVAPTAKARRVVO	12951	571	10	16
ENV	FNGTGPCKN	13608	16	25	DKKFNGTGPCKNVST	12952	276	05	8
ENV	IGPGQTFYA	13609	01	25	SVRIGPGQTFYATGD	12953	355	03	5
ENV	IGSGQAFYV	13610	01	25	RYSIGSGQAFYVTGK	12954	358	01	2
ENV	IRYLNLVNQ	13611	01	25	QTAIRYLNLVNQTEN	12955	400	01	2
ENV	LIGLRIFA	13612	16	25	VGGLIGLRIFAVALS	12956	784	12	19
ENV	LLQYWSQEL	13613	16	25	WWNLLQYWSQELKNS	12957	903	09	14
ENV	LRNLCLFSY	13614	16	25	WDDLRLNLCLFSYHRL	12958	854	11	17
ENV	LVSGFLALA	13615	16	25	SIRLVSGFLALAWDD	12959	842	09	14
ENV	VSGFLALAW	13616	16	25	IRLVSGFLALAWDDL	12960	843	09	14
ENV	FDPIPIHYC	13617	15	23	KVTFDPIPIHYCTPA	12961	252	03	5
ENV	IIFAVLSIV	13618	15	23	GLRIIFAVLSIVNRV	12962	789	13	20
ENV	LINCNTSAI	13619	15	23	EYRLINCNTSAITQA	12963	234	04	9

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	LLNATAIAV	13620	15	23	AVSLLNATAIAVAEG	12964	918	10	16
ENV	LRIIFAVLS	13621	15	23	LIGLRIIFAVLSIVN	12965	787	11	17
ENV	VITQACPKV	13622	15	23	NTSVITQACPKVSFE	12966	241	08	13
ENV	YWNLLQYW	13623	15	23	VLKYWNLLQYWSQE	12967	899	07	11
ENV	FAILKCNDK	13624	14	22	PAGFAILKCNDDKFN	12968	266	09	14
ENV	IFAVLSIVN	13625	14	22	LRIIFAVLSIVNRV	12969	790	13	20
ENV	INCNTSAIT	13626	14	22	YRLINCNTSAITQAC	12970	235	14	22
ENV	LNATAIAVA	13627	14	22	VSLNATAIAVAEGT	12971	919	10	16
ENV	WNSSWSNKS	13628	14	22	NVPWNSSWSNKSLE	12972	693	03	5
ENV	WNASWSNKS	13629	13	21	NVPWNASWSNKS	12973	693	02	3
ENV	ICTTTVPWN	13630	13	20	GKLICTTTVPWNASW	12974	686	06	9
ENV	LLKLTWVGI	13631	13	20	QQHLLKLTWVGKQL	12975	648	13	20
ENV	LYRYKVVEI	13632	13	20	RSELYKYKVVEIKPL	12976	558	05	8
ENV	MELGFLGAA	13633	13	20	LGAMFLGFLGAAGST	12977	600	07	11
ENV	MHSFNCGGE	13634	13	20	EIVMHSFNCGGEFF	12978	430	13	20
ENV	YWSQELKNS	13635	13	20	LLQYWSQELKNSAVS	12979	906	10	16
ENV	IGAVFLGFL	13636	12	19	AVGIGAVFLGFLGAA	12980	595	09	14
ENV	LIAARTVEL	13637	12	19	DFILIAARTVELLGH	12981	870	04	6
ENV	LICTTTVPW	13638	12	19	TQLLNGSLAEGEII	12982	685	06	9
ENV	LLNGSLAEG	13639	12	19	LVWYWGQELKNSAIS	12983	304	03	5
ENV	YWGQELKNS	13640	12	17	FILIAARTVELLGH	12984	906	02	3
ENV	IAARTVELL	13641	11	17	IGALFLGFLGAAGST	12985	871	03	5
ENV	LFLGFLGAA	13642	11	17	SOELKNSAVSLLNAT	12986	600	06	9
ENV	LKNSAVSLL	13643	11	17	KRAVGIGAVFLGFLG	12987	911	08	13
ENV	VGIGAVFLG	13644	11	17	NSAVSLLNATAIAVA	12988	593	11	17
ENV	VSLNATAI	13645	11	17	QTFYATGDIIGDIRQ	12989	916	09	14
ENV	YATGDIIGD	13646	11	17	LDIIAIAVAEGTDRI	12990	365	04	6
ENV	IAIAVAEGT	13647	10	16	PIPIHYCTPAGFAIL	12991	922	02	3
ENV	IHYCTPAGF	13648	10	16	GTLILGLVICSASN	12992	258	08	13
ENV	ILGLVICS	13649	10	16	VDEIWNMTWMEWER	12993	19	03	5
ENV	IWNMTWME	13650	10	16	TLILGLVICSASN	12994	714	01	2
ENV	LGLVICS	13651	10	16	YHRLRDFILIAARTV	12995	20	04	6
ENV	LRDFILIA	13652	10	16	CVKLTPLCVTLDCIN	12996	865	06	9
ENV	LTPLCVTL	13653	10	16	QQHMLQLTVWGIKQL	12997	132	03	5
ENV	MLQLTVWGI	13654	10	16	NESVEINCTRPNNT	12998	648	08	13
ENV	VEINCTRPN	13655	10	16	TVQVRQLLSGIVQQQ	12999	338	02	3
ENV	VROLLSGIV	13656	10	16	WGTLILGLVICSAS	13000	624	08	13
ENV	LILGLVIIC	13657	09	15	LNTVGGHQAAMQMLK	13001	18	07	11
GAG	VGGHQAAMQ	13658	60	94	TETLLVQNANPDCKT	13002	209	47	73
GAG	LLVQNANPD	13659	59	92	TLLVQNANPDCKT	13003	342	26	41
GAG	VQNANPDCK	13660	59	92	TLLVQNANPDCKTIL	13004	344	44	69
GAG	LGLNKIVRM	13661	58	91	WILGLNKIVRMYS	13005	289	55	86
GAG	LSEGAIPQD	13662	58	89	FSALSEGATPQDLNT	13006	193	29	45
GAG	WILGLNKI	13663	57	88	YKRWILGLNKIVRM	13007	286	54	84
GAG	LEEMMTACQ	13664	56	88	GATLEEMMTACQGVG	13008	364	27	42
GAG	IYKRWILGL	13665	55	86	GEYKRWILGLNKI	13009	283	37	58
GAG	IYKRWILG	13666	54	84	VGEYKRWILGLNK	13010	282	37	58
GAG	VSQNPYIVQ	13667	48	83	SSQVSNQNPYIVQNLQ	13011	145	09	19
GAG	WEKIRLRPG	13668	50	78	LDKWEKIRLRPGGKK	13012	13	16	25
GAG	IAGTTSTLQ	13669	46	72	GSDIAGTTSTLQEQI	13013	254	45	70

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
GAG	WASRELERF	13670	46	72	HLVWASRELERFALN	13014	34	17	27
GAG	IPMFALSE	13671	45	70	PEVIPMFALSSEGAT	13015	187	44	69
GAG	MFSALSEGA	13672	45	70	VIPMFALSSEGATPQ	13016	189	43	67
GAG	VIPMFALS	13673	45	70	SPEVIPMFALSSEGA	13017	186	40	63
GAG	MYSVPVSI	13674	41	64	IVRMYSPVSI	13018	297	23	36
GAG	IVRMYSPVS	13675	40	63	LNKIVRMYSPVSILD	13019	294	39	61
GAG	VRMYSPVSI	13676	40	63	NKIVRMYSPVSILD	13020	295	38	59
GAG	YSPVSILDI	13677	40	63	VRMYSPVSILDIRQG	13021	298	23	36
GAG	MTETLLVQN	13678	38	58	KNWMTETLLVQNANP	13022	338	34	53
GAG	WMETLLVQ	13679	37	56	VKNWMTETLLVQNAN	13023	337	34	53
GAG	ISPRTLNAW	13680	36	56	HQAISPRTLNAWVKV	13024	165	27	42
GAG	VKNWMTETL	13681	36	56	TQEVKNWMTETLLVQ	13025	334	14	22
GAG	IKCFNCGKE	13682	34	53	QKRIKCFNCGKEGHL	13026	418	05	8
GAG	IPVGEIYKR	13683	34	53	NPPIPVGEIYKRWII	13027	277	32	51
GAG	YTAVFMQRG	13684	02	50	KGGYTAVFMQRQGNP	13028	399	02	3
GAG	VATLYCVHQ	13685	30	47	YNTVATLYCVHQRIE	13029	81	07	11
GAG	WDRLLHPVHA	13686	29	45	AAEWDRLLHPVHAGPI	13030	230	22	34
GAG	FLQSRPEPT	13687	28	44	PGNFLQSRPEPTAPP	13031	483	27	43
GAG	FKTLRAEQ	13688	27	42	DRFFKTLRAEQATQE	13032	322	16	25
GAG	MVHQAIQSPR	13689	27	42	QQMVHQAIQSPRTL	13033	160	26	41
GAG	VHQAIQSPRT	13690	27	42	QOMVHQAIQSPRTLNA	13034	161	27	42
GAG	YKTLRAEQ	13691	27	42	DRFYKTLRAEQASQE	13035	322	12	19
GAG	VSILDIRQG	13692	25	39	YSPVSILDIRQGPKE	13036	301	24	38
GAG	LAEMSQVT	13693	23	37	ARVLAEMSQVTNSA	13037	384	08	13
GAG	LGIWPSHK	13694	23	36	ANFLGIWPSHKGR	13038	467	22	34
GAG	VKFCNCGKE	13695	23	36	RKTVKFCNCGKEGHI	13039	420	11	11
GAG	YNTVATLYC	13696	23	36	RSLYNTVATLYCVHQ	13040	78	11	17
GAG	LHPVHAGPI	13697	22	34	WDRLLHPVHAGPIAPG	13041	233	15	23
GAG	LYNTVATLY	13698	22	34	LRSLYNTVATLYCVH	13042	77	13	20
GAG	MTDTLLVQN	13699	22	34	KNWMTDTLLVQNANP	13043	338	16	25
GAG	WMTDTLLVQ	13700	22	34	VKNWMTDTLLVQNAN	13044	337	16	25
GAG	IEVKDTKEA	13701	21	33	HQRIEVDKTEALDK	13045	91	07	11
GAG	LQGMVHQA	13702	21	33	VQNLQGMVHQAISP	13046	156	15	23
GAG	MTNNPIPV	13703	20	31	IGWMTNNPIPVGEI	13047	268	16	25
GAG	WMTNNPIPV	13704	20	31	QIGWMTNNPIPVGEI	13048	267	16	25
GAG	IAPQMREP	13705	19	30	AGPIAPQMREP	13049	241	19	30
GAG	VHAGPIAPG	13706	19	30	LHPVHAGPIAPQM	13050	236	14	22
GAG	LPGATLEE	13707	18	28	LRALPGATLEEMMT	13051	358	09	14
GAG	VHAGPIPG	13708	18	28	VHPVHAGPIPGQMR	13052	236	10	16
GAG	IPPGQMR	13709	17	27	AGPIPGQMR	13053	241	16	25
GAG	LSPRTLNAW	13710	17	27	HQAISPRTLNAWVKV	13054	165	10	16
GAG	YRLKHLVVA	13711	17	27	KKKYRLKHLVWASRE	13055	27	13	20
GAG	LGPAAATLEE	13712	16	25	LKALGPAATLEEMMT	13056	358	16	25
GAG	LKALGPAAT	13713	16	25	KTILKALGPAATLEE	13057	355	16	25
GAG	LKDKEPPLA	13714	01	25	QEQLKDKEPPLASLR	13058	532	01	2
GAG	LSGGKLDW	13715	16	25	ASVLSGGKLDWKEI	13059	5	14	22
GAG	MTSNPIPV	13716	16	25	IGWMTSNPIPVGEI	13060	268	06	9
GAG	VKNWMTDTL	13717	16	25	TQDVKNWMTDTLLVQ	13061	334	11	17
GAG	VSILDIKQG	13718	16	25	YSPVSILDIKQGPKE	13062	301	16	25
GAG	WMTSNPIPV	13719	16	25	QIGWMTSNPIPVGEI	13063	267	06	10

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
GAG	FNIVATLYC	13720	15	23	KSIFNTVATLYCVHQ	13064	78	07	11
GAG	IPMFTALSE	13721	15	23	PEVIPMFTALSEGAT	13065	187	13	20
GAG	LASLSLFG	13722	15	23	LYPLASLSLFGNDP	13066	544	06	11
GAG	LERFAVNP	13723	15	23	SRELERFAVNPGLLE	13067	39	14	22
GAG	LFNTVATLY	13724	15	23	LRSLFNTVATLYCVH	13068	77	07	11
GAG	MFTALSEGA	13725	15	23	VIPMFTALSEGATPQ	13069	189	14	22
GAG	WDRVHVPVHA	13726	15	23	AAEWDRVHVPVHAGPI	13070	230	12	19
GAG	IVRMYSPTS	13727	14	22	LNKIVRMYSPTSILD	13071	294	13	20
GAG	LERFALNPG	13728	14	22	SRELERFALNPGLE	13072	39	14	22
GAG	LQEQIAWMT	13729	14	22	TSTLQEQIAWMTGNP	13073	261	05	8
GAG	VHPVHAGPI	13730	14	22	WDRVHVPVHAGPIPPG	13074	233	11	17
GAG	VIPMFTALS	13731	14	22	SPEVIPMFTALSEGA	13075	186	13	20
GAG	VRMYSPTS	13732	14	22	NKIVRMYSPTSILDI	13076	295	13	20
GAG	LGIWPSNK	13733	13	20	ANFLGIWPSNKGPR	13077	467	13	20
GAG	LTSLSLFG	13734	13	20	LYPLTSLSLFGNDP	13078	544	04	7
GAG	MYSPSILD	13735	13	20	IVRMYSPTSILDIRQ	13079	297	12	19
GAG	YKLKHIVA	13736	13	20	KKKYKLKHIVWASRE	13080	27	08	13
GAG	YSPTSILDI	13737	13	20	VRMYSPTSILDIRQG	13081	298	12	19
GAG	LTSLSLFG	13738	12	19	LYPLTSLSLFGNDP	13082	544	04	7
GAG	MMLNIVGGH	13739	12	19	DLNMLNIVGGHQA	13083	204	12	19
GAG	IDVKDTKEA	13740	11	17	HQRIDVKDTKEALDK	13084	91	03	5
GAG	IGWMTSNPP	13741	11	17	QEQIGWMTSNPPPIV	13085	265	09	14
GAG	IPVGDYKR	13742	11	17	NPPVGDYKRWII	13086	277	08	13
GAG	LYPLASLKS	13743	09	17	DKELYPLASLKSIFG	13087	541	06	10
GAG	VHQALSPT	13744	11	17	GQMVHQALSPTLNA	13088	161	07	11
GAG	VNPGLLETS	13745	11	17	RFAVNPGLLETS	13089	45	11	17
GAG	YPLASLSL	13746	08	17	KELYPLASLSLFGN	13090	542	06	9
GAG	FLQNRPEPT	13747	10	16	PGNFLQNRPEPTAPP	13091	483	10	16
GAG	IMMQSNFK	13748	10	16	AAAIMMQSNFKGPR	13092	405	01	25
GAG	LAEMSQQV	13749	10	16	ARVLAEMSQQVQSN	13093	384	02	3
GAG	LNPGLETA	13750	10	16	ANFLGKIWPSSKGRP	13094	467	10	16
GAG	YPLASLSL	13751	10	16	RFALNPGLLETAEGC	13095	45	08	13
GAG	WQNYTPGPG	13752	07	15	KELYPLASLSLFGN	13096	542	04	6
NEF	VRQVPLRP	13753	52	83	FPDWQNYTPGPGIRY	13097	200	15	23
NEF	VPLRPMYK	13754	48	75	GFPVPRQVPLRPMY	13098	93	36	56
NEF	LTFGWCFKL	13755	46	73	RQVPLRPMYKGF	13099	98	07	11
NEF	ILDLWVYHT	13756	39	61	RYPLTFGWCFKLVVP	13100	216	15	24
NEF	WCFKLVVD	13757	34	53	RQEILDLWVYHTQGY	13101	182	12	19
NEF	LWVYHTQGY	13758	26	41	TFGWCFKLVVDPRE	13102	222	07	11
NEF	WSKSSVIGW	13759	21	33	ILDLWVYHTQGYFPD	13103	186	21	33
NEF	ILDLWVYNT	13760	20	31	GKWSKSSVIGWPAI	13104	2	05	8
NEF	LLHPMSQHG	13761	19	30	RQDILDLWVYNTQGY	13105	182	05	8
NEF	LLHPICQHG	13762	17	27	NNCLLHPMSQHGMD	13106	254	06	9
NEF	IRYPLTFGW	13763	16	25	NNSLLHPICQHGMD	13107	254	04	6
NEF	ITSNTAAT	13764	13	20	GPGRYPLTFGWCFK	13108	210	06	9
NEF	LEKHGATS	13765	13	20	HGATSSNTAATNAD	13109	61	10	16
NEF	LWVYHTQGF	13766	13	20	SRDLKXHGATSSNT	13110	50	13	20
NEF	MTYKGAIDL	13767	12	19	ILDLWVYHTQGFPPD	13111	186	13	20
NEF	LVPDPREV	13768	11	17	LRPMYKGAIDLSPF	13112	103	06	9
NEF		13769	11	17	CFKLVDPDREVEEA	13113	226	08	13

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
NEF	VGWPAIRER	13770	10	17	SSIVGWPAIRMR	13114	8	03	5
NEF	WCFKLVPE	13771	11	17	TFGWCFLVPVEPEK	13115	222	04	6
NEF	FDSRLAFIH	13772	10	16	EWRFDSRLAFHVAR	13116	307	02	3
NEF	FKLVVPDPR	13773	10	16	GWCFKLVVPDPREVE	13117	224	10	16
NEF	VPLRPMTEK	13774	10	16	RPQVPLRPMTEKGF	13118	98	04	6
POL	LLDTGADDT	13775	63	98	KEALLDTGADDTVLE	13119	107	37	58
POL	WMGYELHPD	13776	63	98	PFLWMGYELHPDKWT	13120	415	60	94
POL	YQYNVLPQG	13777	63	98	GIRYQYNVLPQWKG	13121	330	52	81
POL	FRKYTAFTI	13778	61	97	DKDFRKYTAFTIPSI	13122	310	10	16
POL	WTVNDIQKL	13779	62	97	KDSWTVNDIQKLVGK	13123	438	43	67
POL	LDCTHLEK	13780	61	95	IWQLDCTHLEKIL	13124	812	29	45
POL	LDVGDAYFS	13781	61	95	VTVLDVGDAYFSVPL	13125	295	50	78
POL	MDDLTVGSD	13782	61	95	YQYMDLTVGSDLEI	13126	370	57	89
POL	VIPAETGQE	13783	61	95	EAEVIPAETGQETAY	13127	837	57	90
POL	WKEGAVVI	13784	61	95	KLLWKEGAVVIQDN	13128	992	53	83
POL	WQLDCTHLE	13785	61	95	PGIWQLDCTHLEGI	13129	810	32	50
POL	VDFRELNR	13786	60	94	RKLVDRELNRKTOD	13130	261	57	89
POL	WPKMIGGI	13787	60	94	PGKWKPKMIGGIGF	13131	126	56	61
POL	IWQLDCTHIL	13788	59	92	SPGIWQLDCTHLEK	13132	809	26	41
POL	VAVHVASGY	13789	59	92	IILVAVHVASGYIEA	13133	824	339	66
POL	IGGYASGER	13790	58	91	PQGWKGSPIFQSSM	13134	940	37	59
POL	YALGHQAQ	13792	58	89	KGIGGYASGERIID	13135	690	39	61
POL	FWEVOLGIP	13793	57	89	DSQYALGIIQAQPK	13136	273	52	81
POL	IKKKDSTKW	13794	57	89	TQDFWEVOLGIPHPA	13137	249	36	56
POL	LGIIQAQPD	13795	57	89	VFAIKKKDSTKWRL	13138	692	39	61
POL	LGIIHPAGL	13796	56	89	QYALGHQAQPKSE	13139	278	51	80
POL	VNTPLVKL	13797	57	89	EVQLGIIHPAGLKKK	13140	606	50	79
POL	VTVLDVGDA	13798	57	89	WEFVNTPLVKLWYQ	13141	292	49	77
POL	FPISPIETV	13799	56	88	KKSVTVLDVGDAYFS	13142	183	52	83
POL	ISPIETVPV	13800	56	88	TLNFPISPIETVPVK	13143	185	52	81
POL	FVNTPLVK	13801	55	86	NFPISPIETVPVKLK	13144	605	50	78
POL	LNFPISPIE	13802	55	86	WEFVNTPLVKLWY	13145	181	53	83
POL	WEFVNTPL	13803	54	86	GCTLNFPISPIETVP	13146	603	49	77
POL	IQNFRVYVR	13804	52	84	IPEWEFVNTPLVKL	13147	969	32	51
POL	LVGPTPVI	13805	54	84	ITKIQNFRVYVRDSR	13148	160	51	80
POL	VQLGIIHPA	13806	54	84	GTVLVGLGPTPVIIGR	13149	276	53	83
POL	WQATWPIEW	13807	54	84	FWEVQLGIIHPAGLK	13150	595	19	30
POL	IETVPVKLK	13808	53	83	TEYWQATWPIEWEFV	13151	188	51	80
POL	IGTVLVGPT	13809	53	83	ISPIETVPVKLKPGM	13152	156	22	34
POL	LVAVHVASG	13810	53	83	KKAIGTVLVGPTPVN	13153	823	26	41
POL	VLVGPTPVN	13811	53	83	KIILVAVHVASGYIE	13154	832	45	70
POL	YIEAEVIPA	13812	53	83	IGTVLVGPTPVIIG	13155	374	52	81
POL	YVGSDELIG	13813	52	81	ASGYIEAEVIPAETG	13156	828	52	81
POL	MDGPKVKQW	13814	52	81	DDLVVGSDELIGQHR	13157	199	47	73
POL	VASGYIAE	13815	52	81	KPGMDGPKVKQWPPLT	13158	205	45	80
POL	VGPTPVNII	13816	52	81	AVHVASGYIAEVIP	13159	974	29	45
POL	VKQWPLTEE	13817	52	81	TVLVGPTPVIIGRN	13160	398	23	36
POL	VYRDSKDP	13818	52	81	GPKVKQWPLTEEKIK	13161			
POL	WGFTTPDKK	13819	52	81	NFRVYRDSRDPPIWK	13162			
					LLRWGFTTPDKKHQK	13163			

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	VVIQYMDIDL	13820	51	80	PEVIYQYMDLLVYG	13164	365	23	36
POL	LKKKKSIV	13821	49	78	PAGLKKKKSIVTLVDV	13165	286	46	72
POL	VPRRKAKIV	13822	50	78	IKVPRRKAKIIRDY	13166	1010	41	64
POL	FPQITLWQR	13823	49	77	SFSFQITLWQRPLV	13167	84	09	14
POL	VWGGTKPKF	13824	47	73	ESVIWGGTKPKFRLP	13168	570	23	37
POL	VYDGAANRE	13825	46	72	ETFYVDGAANRETKL	13169	630	24	38
POL	FNKLTGKY	13826	45	70	QEPFKNLTKGYAKM	13170	535	15	23
POL	IQTRELQKQ	13827	45	70	ATDIQTKELQKQITK	13171	957	24	38
POL	YQKQMGDD	13828	45	70	IRDYQKQMGDDCVA	13172	1021	41	64
POL	WRAMASDFN	13829	43	67	HSNWRAMASDFNLP	13173	768	31	768
POL	ISKIGFNP	13830	42	66	EGKISKIGFNPYNT	13174	233	40	48
POL	LTIQIGCTLN	13831	41	64	RNLLTIQIGCTLNFI	13175	174	21	63
POL	IQAQPKDS	13832	40	63	ALGIIQAQPKDSESE	13176	694	38	59
POL	LPEKDSWTV	13833	40	63	PIVLPKDSWTVNDI	13177	432	13	20
POL	FQSSMTKIL	13834	38	59	PAIFQSSMTKILEPF	13178	346	32	50
POL	FTIPSINNE	13835	38	59	YTAFTIPSINNETPG	13179	316	36	56
POL	IFQSSMTKI	13836	38	59	SPAIQSSMTKILEP	13180	345	33	52
POL	IEQLIKKE	13837	37	58	VSQIEQLIKKEKVV	13181	710	19	30
POL	LSWVPAHKG	13838	37	58	KVYLSWVPAHKGIGG	13182	722	23	37
POL	YLSWVPAHK	13839	37	58	EKVYLSWVPAHKGIG	13183	721	15	24
POL	YTAFTIPSI	13840	37	58	FRKYTAFTIPSINNE	13184	313	37	59
POL	IIATDIQTK	13841	35	55	IIIDIATDIQTKELQ	13185	952	22	34
POL	IKWGPALKL	13842	35	55	RDPIWKGPALKLLWKG	13186	983	34	53
POL	LQKQITKIQ	13843	35	55	TKELQKQITKIQNFR	13187	962	29	46
POL	LKEALDTG	13844	34	53	GGQLKEALLDTGADD	13188	103	31	48
POL	VYLSWVPAH	13845	33	52	KEKVYLSWVPAHKG	13189	720	15	23
POL	FILKLGRW	13846	32	50	TAYFILKLGRWPVK	13190	849	27	42
POL	LEKILVA	13847	31	48	CTHLEKILVAVHV	13191	817	30	47
POL	YFILKLGR	13848	31	48	ETAYFILKLGRWPV	13192	848	30	47
POL	ILVAVHVA	13849	30	47	EGKILVAVHVASGY	13193	821	30	47
POL	IWGKTPKFR	13850	30	47	SIVIWGKTPKFRPLI	13194	571	22	34
POL	LGRWPVKV	13851	30	47	ILKLGRWPVKVIHT	13195	853	19	30
POL	VVAKEIVAS	13852	30	47	LPPVVAKEIVASCDK	13196	780	21	33
POL	IDIATDIQ	13853	29	45	ERIDIATDIQTK	13197	950	22	34
POL	IDIATDI	13854	29	45	GERIDIATDIQTK	13198	949	23	36
POL	IIGRNMLTQ	13855	29	45	PVNIIGRNMLTQIGC	13199	168	11	17
POL	IKVKQLCKL	13856	29	45	YAGIKVKQLCKLLRG	13200	460	18	28
POL	VDKLVSIGI	13857	29	45	NEQVDKLVSIGIRKV	13201	737	26	41
POL	IVGAETFYV	13858	28	44	KEPIVGAETFYVDGA	13202	623	16	25
POL	LPPVVAKEI	13859	28	44	DFNLPPVVAKEIVAS	13203	777	26	41
POL	WTVQPIQLP	13860	28	44	PKWTVQPIQLPEKD	13204	425	13	20
POL	FNLPVVAKE	13861	27	42	ASDFNLPPVVAKEIV	13205	775	25	39
POL	FTSAAVKAA	13862	27	42	GSNFTSAAVKAAACW	13206	870	25	39
POL	LALQDSGLE	13863	27	42	AHLALQDSGLEVNI	13207	673	15	23
POL	LPPVVAKEI	13864	27	42	DFNLPPVVAKEIVAS	13208	777	20	31
POL	LQDSGLEVN	13865	27	42	HLALQDSGLEVNIVT	13209	675	13	20
POL	FNLPVVAKE	13866	26	41	ASDFNLPPVVAKEIV	13210	775	21	33
POL	IGQHRAKIE	13867	26	41	DLEIGQHRAKIEELR	13211	381	23	36
POL	IIGRNLLTQ	13868	26	41	PVNIIGRNLLTQIGC	13212	168	21	33
POL	LEVNIIVTDS	13869	26	41	DSGLEVNIIVTDSQYA	13213	680	26	41

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	LRGAKALTD	13870	26	41	CKLLRGAKALTDIVP	13214	469	12	19
POL	LVSSGIRKV	13871	26	41	VDKLVSSGIRKVLFL	13215	740	25	39
POL	FLKLKAGRW	13872	25	39	TAYFLKLKAGRWPK	13216	849	19	30
POL	LALQDSGE	13873	25	39	AHLALQDSGSEVNI	13217	673	08	13
POL	LQDSGSEVN	13874	25	39	HLALQDSGSENVIT	13218	675	08	13
POL	VKVIHTDNG	13875	25	39	RWPVKVIHTDNGSNF	13219	859	21	33
POL	WPKVVIHTD	13876	25	39	AGRWPVKVIHTDNGS	13220	857	20	31
POL	YFLKLKAGR	13877	25	39	ETAYFLKLKAGRPV	13221	848	24	38
POL	ICGKKAIGT	13878	24	38	LIEICGKKAIGTVLV	13222	150	12	19
POL	IVAKEIVAS	13879	24	38	LPPIVAKAIVASCDK	13223	780	22	34
POL	LRWGFTTPD	13880	24	38	QHLLRWGFTTPDKKH	13224	396	12	19
POL	LEGKVLVA	13881	23	36	CTHLEGKVLVAHV	13225	817	23	36
POL	LKWGFTTPD	13882	23	36	EHLKKGWGTTPDKKH	13226	396	13	20
POL	VILVAHVVA	13883	23	36	EGKVLVAHVAVASGY	13227	821	21	33
POL	LAWVPAHKG	13884	22	34	KVYLAWVPAHKGIGG	13228	722	20	32
POL	YDQILIEIC	13885	22	34	VRQYDQILIEICGKK	13229	143	08	13
POL	YLAWVPAHK	13886	22	34	EKVYLAWVPAHKGIG	13230	721	20	32
POL	IGQIRTKIE	13887	21	33	DLEIGQIRTKIEELR	13231	381	19	30
POL	IGRNLLTQI	13888	21	33	VNIIGNLLTQIGCT	13232	169	21	33
POL	LWQRPVTV	13889	21	33	QITLWQRPVTVIKIG	13233	89	11	17
POL	VSLTETTNQ	13890	21	33	QKVVSLETETTNQKTE	13234	656	10	16
POL	VYLAWVPAH	13891	21	33	KEKVYLAWVPAHKG	13235	720	20	31
POL	ICGHKAIGT	13892	20	31	LIEICGHKAIGTVLV	13236	150	10	16
POL	LRGFKALTE	13893	19	30	CKLLRGFKALTEVIP	13237	469	11	17
POL	LVNQIEQL	13894	19	30	ESELVNQIEQLIKK	13238	706	13	20
POL	LVSQIEQL	13895	19	30	ESELVSQIEQLIKK	13239	706	18	28
POL	YFSPVLDKD	13896	18	29	GDAYFSPVLDKDFRK	13240	301	18	28
POL	IGRNMLTQI	13897	18	28	VNIIGNMLTQIGCT	13241	169	12	19
POL	IKVRQLCKL	13898	18	28	YPGIKVRQLCKLLRG	13242	460	13	20
POL	LWKGPAKLL	13899	18	28	RDPLWKGPAKLLWKG	13243	983	13	20
POL	LWQRPVTV	13900	18	28	QITLWQRPVTVIKIG	13244	89	09	14
POL	YAGIKVKQL	13901	18	28	SQIYAGIKVKQLCKL	13245	457	18	28
POL	IWGKTPKFK	13902	17	27	SIVIWGKTPKFKLPI	13246	571	17	27
POL	LREHLLKKG	13903	17	27	IEELREHLLKKGWFTT	13247	391	12	19
POL	VQIQLPEK	13904	17	27	KWTVQIQLPEKDSW	13248	427	13	20
POL	WQRPVTVIK	13905	17	27	ITLWQRPVTVIKIG	13249	90	11	17
POL	IIQAQDRS	13906	16	25	ALGIIQAQDRSESE	13250	694	12	19
POL	LQAIHLALQ	13907	16	25	KTELQAIHLALQDSG	13251	668	15	23
POL	LVEICTEME	13908	15	24	IKALVEICTEMEKEG	13252	218	15	23
POL	LRQHLLRWG	13909	15	23	IEELRQHLLRWGFTT	13253	391	12	19
POL	LTQLGCTLN	13910	15	23	RNMLTQLGCTLNFP	13254	174	10	16
POL	LVSAGIRKV	13911	15	23	VDKLVSAGIRKVLFL	13255	740	14	22
POL	VDKLVASAGI	13912	15	23	NEQVDKLVASAGIRKV	13256	737	14	22
POL	YPGIKVRQL	13913	15	23	SQIYPGIKVRQLCKL	13257	457	12	19
POL	FRKQNPDI	13914	14	22	LEPERKQNPDIYQ	13258	357	14	22
POL	FSPQITLW	13915	14	22	TVSFSFPQITLWQRP	13259	77	05	10
POL	FSTTTVKA	13916	14	22	GSNFTSTTVKAACWW	13260	870	11	17
POL	IASDIQTK	13917	14	22	IIDIASDIQTKELQ	13261	952	11	17
POL	LAGRWPKTK	13918	14	22	LLKLAGRWPKTKTHT	13262	853	09	14
POL	VQKIATESI	13919	14	22	TEAVQKIATESIVIV	13263	561	10	16

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	FTIPSTNNE	13920	13	20	YTAFTIPSTNNETPG	13264	316	13	20
POL	LEDINLPKG	13921	13	20	DTVLEDINLPKGWKP	13265	117	13	20
POL	LTDIVPLTE	13922	13	20	AKALTDIVPLTEAE	13266	475	08	13
POL	LVTIKIGGQ	13923	13	20	QRPLVTIKIGGQKE	13267	94	13	20
POL	MARGAHTNDV	13924	13	20	YARMARGAHTNDVKQL	13268	546	12	19
POL	VKTHITDNG	13925	13	20	RWPVKTHITDNGSNF	13269	859	09	14
POL	VQPIVLPEK	13926	13	20	KWTVQPIVLPEKDSW	13270	427	12	19
POL	WPKVKTHTD	13927	13	20	AGRWPKVKTHTDNGS	13271	857	09	14
POL	WQRPVTVK	13928	13	20	ITLWQRPVTVKIGG	13272	90	09	14
POL	WTVQPIVLP	13929	13	20	PDKWTVPVLPPEKD	13273	425	12	19
POL	YTAFTIPST	13930	13	20	FRKYTAFTIPSTNNE	13274	313	13	21
POL	IDIASDIQ	13931	12	19	ERIIDIASDIQIKE	13275	950	11	17
POL	IDIASDI	13932	12	19	GERIIDIASDIQTK	13276	949	11	17
POL	IVDIIATDI	13933	12	19	GERIVDIIATDIQTK	13277	949	10	16
POL	LEEINLPKG	13934	12	19	DTVLEEINLPKGWKP	13278	117	11	17
POL	LQAIYLALQ	13935	12	19	KTELQAIYLALQDSG	13279	668	11	17
POL	LOKQIKIQ	13936	12	19	TKELQKQIKIQNFR	13280	962	09	14
POL	VDIATDIQ	13937	12	19	ERIVDIATDIQIKE	13281	950	10	16
POL	YDQIPEIC	13938	12	19	VRQYDQIPEICGKK	13282	143	05	8
POL	FNFPQITLW	13939	11	17	VPTFNFPQITLWQRP	13283	79	01	17
POL	IGRNMLTQL	13940	11	17	VNIIGRNMLTQLGCT	13284	169	10	16
POL	ISRIGPENP	13941	11	17	EGKISRIGPENPYNT	13285	233	10	16
POL	LTEVIPLE	13942	11	17	TKALTEVIPLETEAE	13286	475	10	16
POL	MESIVWGK	13943	11	17	KIAMESIVWGKTPK	13287	566	07	11
POL	VPRKVKII	13944	11	17	IKVVPRKVKIIRDY	13288	1010	08	13
POL	VSFSPQIT	13945	08	17	QGTVSFSFPQITLWQ	13289	75	05	8
POL	WYQLETEPI	13946	11	17	VKLWYQLETEPIVGA	13290	615	04	6
POL	YPIKVKQL	13947	11	17	SOIYPGIKVKQLCKL	13291	457	09	14
POL	FPQGEAREF	13948	10	16	NLAFFQGEAREFPPE	13292	5	05	8
POL	LIEALLDTG	13949	10	16	GGQLIEALLDTGADD	13293	103	09	14
POL	VSLDITNQ	13950	10	16	QKVVSLLDITNQKTE	13294	656	09	14
POL	WETWWTDYW	13951	10	16	KETWETWWTDYWQAT	13295	587	09	14
POL	YAKMRTAHT	13952	10	16	TGKYAKMRTAHTNDV	13296	543	03	5
POL	YKNLKTGKY	13953	10	16	QEPYKNLKTGKYARM	13297	535	03	14
REV	LQLPLERL	13954	36	56	PVPLQLPLERLTLT	13298	74	13	20
REV	VPLQLPLE	13955	36	56	AEPVPLQLPLERLT	13299	72	10	16
REV	LYQSNPPPS	13956	18	28	IKFLYQSNPPPSPEG	13300	21	04	6
REV	VRIKILYQ	13957	16	25	LKAVRIKILYQSNP	13301	13	06	9
REV	YQSNPPSP	13958	12	19	KFLYQSNPPPSPEGT	13302	22	05	8
REV	LQLPLERL	13959	11	17	PVPLQLPLERLRLD	13303	74	04	6
REV	VPLQLPIE	13960	11	17	AEPVPLQLPIERLR	13304	72	04	6
TAT	WNHPGSQPK	13961	15	23	LEPWNIHPGSQPKTAC	13305	11	11	17
TAT	FLNKGLGIS	13962	14	22	QVCFNLKGLGISYGR	13306	38	04	6
TAT	WKIIPGSQPK	13963	13	20	LEPWKHPGSQPKTAC	13307	11	11	17
TAT	YCKKCCFHC	13964	11	17	NNCYCKKCCFHCQVC	13308	26	04	6
TAT	YCKKCCYHC	13965	11	17	TNCYCKKCCYHCQVC	13309	26	02	3
TAT	WNHPGSQPT	13966	10	16	LEPWNIHPGSQPTTAC	13310	11	07	11
VIF	MIVWQVDRM	13967	46	72	WQVMIVWQVDRMRIR	13311	5	28	44
VIF	WQVMIVWQV	13968	43	67	ENRWQVMIVWQVDRM	13312	2	41	64
VIF	WQVDRMRIR	13969	34	53	MIVWQVDRMRIRTWK	13313	8	14	22

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VIF	LOYLALTAL	13970	33	52	VGSLOYLALTALIKP	13314	147	14	22
VIF	LGHGVSEW	13971	31	48	DWHLGHGVSEWRRLR	13315	81	11	17
VIF	VDRMRIRTW	13972	31	48	VWQVDRMRIRTWNSL	13316	10	15	23
VIF	YFDCFESA	13973	28	44	HLYYFDCFESAIRN	13317	113	08	13
VIF	YWGLHTGER	13974	28	44	ITTYWGLHTGERDWH	13318	68	14	22
VIF	IRTWNSLVK	13975	27	42	RMRTWNSLVKHHM	13319	15	12	19
VIF	LQGGVSEW	13976	26	41	DWHLQGGVSEWRKK	13320	81	07	11
VIF	LVKHHMYVS	13977	21	33	WNSLVKHHMYVSKKA	13321	21	07	11
VIF	IPLGEARLV	13978	19	30	EVHPLGEARLVVRT	13322	54	05	8
VIF	LVKHHMYIS	13979	19	30	WKS LVKHHMYISGKA	13323	21	05	8
VIF	YLALTALIK	13980	16	25	SLQYLALTALIKPKK	13324	149	11	17
VIF	IRTWKSLVK	13981	15	23	RMRTWKS LVKHHM	13325	15	14	22
VIF	LADQLHLY	13982	15	23	DPDLADQLHLYYFD	13326	104	07	11
VIF	LALTALIKP	13983	15	23	LQYLALTALIKPKKI	13327	150	08	13
VIF	VDPLADQL	13984	15	23	STOVDPGLADQLIHL	13328	100	04	6
VIF	LYYFDCFE	13985	14	22	LHLYYFDCFESAI	13329	111	14	22
VIF	FSESARKA	13986	13	20	FDCFESARKAILG	13330	117	10	16
VIF	LADQLHMH	13987	13	20	EPLADQLHMHYFD	13331	104	08	13
VIF	WQVDRMKIR	13988	13	20	LIVWQVDRMKIRTW	13332	8	09	14
VIF	FSDSAIRKA	13989	12	19	FDCFSDSAIRKAILG	13333	117	05	8
VIF	FSESARNA	13990	12	19	FDCFSESARNAIG	13334	117	12	19
VIF	IVSPRCEYQ	13991	12	19	LGHIVSPRCEYQAGH	13335	130	06	9
VIF	LOYLALAAL	13992	12	19	VGSLOYLALAALITP	13336	147	04	6
VIF	VDRMKIRTW	13993	12	19	VWQVDRMKIRTWNSL	13337	10	12	19
VIF	YWGLQTGER	13994	12	19	IKTYWGLQTGERDWH	13338	68	08	13
VIF	IPLGARLV	13995	11	17	EVHPLGARDARLVIT	13339	54	06	9
VIF	LQYLALKAL	13996	11	17	VGSLOYLALKALVTP	13340	147	08	13
VIF	WQVDRMRIN	13997	11	17	MIVWQVDRMRINTWK	13341	8	08	13
VIF	IKPKKIKPP	13998	10	16	TALIKPKKIKPPPS	13342	156	08	13
VIF	VDRMRINTW	13999	10	16	VWQVDRMRINTWKS	13343	10	09	14
VPR	IGCQHSRIG	14000	46	72	HFRIGCQHSRIGITR	13344	71	08	13
VPR	WTLELEEL	14001	42	69	YNEWTLLEELKSE	13345	15	12	19
VPR	ILQQLFIH	14002	37	58	IIRLQQLFIHFRI	13346	60	31	48
VPR	FIHFRIGQ	14003	30	47	QLLFIHFRIGCQHSR	13347	66	29	45
VPR	YNEWTLLEL	14004	30	47	REPYNWTLLELEEL	13348	12	27	42
VPR	FPRPWLHGL	14005	24	38	VRHFRPWLHGLGQH	13349	31	12	19
VPR	WEGVEAIR	14006	18	28	GDTWEGVEAIRILQ	13350	51	14	22
VPR	LEELKSEAV	14007	16	25	LELEELKSEAVRHF	13351	20	15	23
VPR	WAGVEAIR	14008	16	25	GDTWAGVEAIRILQ	13352	51	15	23
VPR	YGDTWAGVE	14009	16	25	YETYGDTWAGVEAII	13353	47	16	25
VPR	IGCRHSRIG	14010	12	19	HFRIGCRHSRIGITR	13354	71	03	5
VPR	FIHFRIGR	14011	11	17	QLLFIHFRIGCRHSR	13355	66	11	17
VPR	FVHFRIGCQ	14012	11	17	QLLFVHFRIGCQHSR	13356	66	10	16
VPR	YGDTWTGVE	14013	11	17	YETYGDTWTGVEAII	13357	47	04	6
VPR	FPRPWLHSL	14014	10	16	VRHFRPWLHSLGQH	13358	31	05	8
VPR	WALELEEL	14015	09	15	YNEWALELEELKNE	13359	15	03	5
VPU	LVTLLSSSK	14016	01	50	EEWLVTLLSSSKLDQ	13360	87	01	2
VPU	VTLSSSKL	14017	01	50	EWLVTLSSSKLDQ	13361	89	01	2
VPU	IIAIVVWTI	14018	23	36	VVAIIAIVVWTIVFI	13362	20	02	3
VPU	VDYRIVIVA	14019	01	33	LAKVDYRIVIVAFIV	13363	5	01	25

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VPV	LRQKIDRL	14020	17	27	RKILRQRKIDRLIDR	13364	44	11	17
VPV	IVVWTIVFI	14021	15	23	IIAIVVWTIVFIEYR	13365	27	07	11
VPV	VVWTIVFIE	14022	14	22	IAIVVWTIVFIEYRK	13366	28	06	9
VPV	IEYRKILRQ	14023	13	21	IVFIEYRKILRQRKI	13367	36	07	11
VPV	ILAIVALVV	14024	11	17	SLYILAIVALVVAIL	13368	3	01	2
VPV	WTIVFIEYR	14025	10	16	IVVWTIVFIEYRKIL	13369	30	05	8
VPV	LAIVALVVA	14026	09	15	LQILAIVALVVAII	13370	4	02	3

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VSTQLLNG	13520	KPVVSTQLLLNGSLA	12864								
VVSTQLLN	13521	IKPVVSTQLLLNGSL	12865								
LTWVGKQL	13522	LLQLTVWVGKQLQAR	12866	0.0840		0.0096		0.0190		0.0750	
LLSGIVQQ	13523	ARQLLSGIVQQSNL	12867								
WATHACVPT	13524	HNWVWATHACVPTDPN	12868								
LGAAGSTMG	13525	LGFLGAAGSTMGAAS	12869								
VRQGYSPLS	13526	VNRVRQGYSPLSFQT	12870	0.0032		-0.0014		0.0230		-0.0010	
LLNLGLAE	13527	STQLLLNGSLAEEV	12871								
VKLTPLCVT	13528	KPCVKLTPLCVTLNC	12872								
LRAIEAOQH	13529	NNLLRAIEAOQHLLQ	12873	0.0280				0.0150			
VSTVQCTHG	13530	CKNVSTVQCTHGKIP	12874								
LGIWGCSGK	13531	QQLLGIWGCSGKLC	12875								
LWDQSLKPC	13532	IISLWDQSLKPCVKL	12876								
LGFLGAAGS	13533	AVFLGFLGAAGSTMG	12877	0.0057		0.0061		0.0096		0.0059	
VWATHACVP	13534	VHNVWATHACVPTDP	12878								
WGKQLQAR	13535	LTWVGKQLQARVLA	12879								
LWYIKIFIM	13536	TNWLWYIKIFIMIVG	12880								
FCASDAKAY	13537	TTLFCASDAKAYDTE	12881								
IVGGLIGLR	13538	FIMIVGGLIGLRIVF	12882								
IFIMIVGGL	13539	YIKIFIMIVGGLIGL	12883								
VYGVVPVWK	13540	WVTVYGVVPVWKEAT	12884	0.0790	6.1000	0.0700	0.0043	0.0180	8.2000	-0.0010	0.0098
IKQLQARVL	13541	VWVGKQLQARVLA	12885								
IKIFIMIVG	13542	LWYIKIFIMIVGGLI	12886								
MGAASITLT	13543	GSTMGAASITLTVQA	12887								
YIKIFIMIV	13544	WLWYIKIFIMIVGGL	12888								
ITGLLLTRD	13545	SSNITGLLLTRDGGK	12889								
IPHYCAPA	13546	FEPIPHYCAPAGFA	12890								
MIYGLIGL	13547	IFIMIVGGLIGLRIV	12891								
VQARQLLSG	13548	TLTVQARQLLSGIVQ	12892								
FEPIPHYC	13549	KVSFEPIPHYCAPA	12893								
LRSLCLFSY	13550	WDDLRLSLCLFSYHRL	12894								
MWKNMVEQ	13551	NFMWKNMVEQMHIE	12895								
VHNVWATHA	13552	DTEVHNVWATHACVP	12896								
WKNNMVEQM	13553	FNMWKNMVEQMHIED	12897								
YYGVVPWKE	13554	VTVYGVVPVWKEATT	12898								
LLQLTVWGI	13555	QQHLLQLTVWGIKQL	12899	0.0087	0.7500	0.0270	-0.0043	0.0071	0.2700	0.0021	0.4900
IEPLGVAPT	13556	VVKIEPLGVAPTAK	12900	1.1000		0.0580		0.0330		0.0036	
IKPVVSTQL	13557	THGKIPVSVSTQLLN	12901								
LQARVLA	13558	IKQLQARVLAVERYL	12902								
WDDLRLSL	13559	ALAWDDLRLSLCLFSY	12903								
IINIHTPIR	13560	SRPINIHTPIHREKR	12904								
INIHTPIRE	13561	RPINIHTPIHREKRA	12905								
ITQACPKVS	13562	TSVITQACPKVSFEP	12906								
IVQQSNLL	13563	LSGIVQQSNLLRAI	12907								
LGNNSTNST	13564	NKTLGNNSTNSTLGN	12908								
VISTRTHRE	13565	ARPVISTRTHREKRA	12909								
WRWGTLFLG	13566	QNLWRWGTLFLGMLM	12910								
WRWGTMLLG	13567	QHLWRWGTMLLGMLM	12911								
FAYLSIVNR	13568	RIVFAVLSIVNRVQ	12912								
LLNGLAE	13569	TQLLNGSLAEEVV	12913								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VSTQLLNG	13520	KPVVSTQLLLNGSLA	12864					
VVSTQLLN	13521	IKPVVSTQLLLNGSL	12865					
LTVWGKQL	13522	LLQLTVWGKQLQAR	12866		0.0180			
LLSGVQQQ	13523	ARQLLSGIVQQSNL	12867					
WATHACVPT	13524	HNWATHACVPTDPN	12868					
LGAAGSTMG	13525	LGFLGAAGSTMGAAS	12869					
VRQYSPLS	13526	VNRVRQYSPLSFQT	12870		-0.0007			
LLNGSLAE	13527	STQLLLNGSLAEFV	12871					
VKLTPLCVT	13528	KPCVKLTPLCVTLNC	12872					
LRAEAOQH	13529	NNLLRAEAOQHLLQ	12873		0.0150			
VSTVQCTHG	13530	CKNVSTVQCTHGKIP	12874					
LGIWGCCKG	13531	QQLLGIWGCCKGLIC	12875					
LWDQSLKPC	13532	IISLWDQSLKPCVKL	12876					
LGFLGAAGS	13533	AVFLGFLGAAGSTMG	12877					
VWATHACVP	13534	VHNWATHACVPTDIP	12878					
WGKQLQAR	13535	LTVWGKQLQARVLA	12879					
LWYIKIFIM	13536	INWLWYIKIFIMIVG	12880					
FCASDAKAY	13537	TTLFCASDAKAYDIE	12881					
IVGGLIGLR	13538	FIMIVGGLIGLRIV	12882					
IFIMIVGGL	13539	YIKIFIMIVGGLIGL	12883					
VYGVVWVK	13540	WVTVYGVVWVWKEAT	12884	-0.0004	0.0310	0.0049	0.4600	
IKQLQARVL	13541	VWGKQLQARVLA	12885					
IKIFIMIVG	13542	LWYIKIFIMIVGGLI	12886					
MGAASITLT	13543	GSTMGAASITLTVQA	12887					
YIKIFIMIV	13544	WLWYIKIFIMIVGGL	12888					
ITGLLITRD	13545	SSNTITGLLITRDGK	12889					
IPHYCAPA	13546	FEPIPHYCAPAGFA	12890					
MVGGGLIGL	13547	IFIMIVGGLIGLRIV	12891					
VQARQLLSG	13548	LTVQARQLLSGIVQ	12892					
FEPIPHYC	13549	KVSFEPIPHYCAPA	12893					
LRSLCLFSY	13550	WDDLRLSLCLFSYHRL	12894					
MWKNMVEQ	13551	NFNMWKNMVEQMHE	12895					
VHNWATHA	13552	DTEVHNWATHACVIP	12896					
WKNMVEQM	13553	FNMWKNMVEQMHE	12897					
YGVVWVKE	13554	VTVYGVVWVWKEATT	12898					
LLQLTVWGI	13555	QQHLLQLTVWGKQL	12899	0.0180	0.0160	0.0210	0.5100	
IEPLGVAPT	13556	VVKIEPLGVAPTAK	12900		0.3900			
IKPVVSTQL	13557	THGKIPVSTQLLN	12901					
LOARVLAVE	13558	IKQLQARVLAVEYL	12902					
WDDLRLSLCL	13559	ALAWDDLRLSLCLFSY	12903					
IIHITPHR	13560	SRPINIHTPHREKR	12904					
IIHITPHRE	13561	RPINIHITPHREKRA	12905					
ITQACPKVS	13562	TSVITQACPKVSFEP	12906					
IVQQSNLL	13563	LSGIVQQSNLLRAI	12907					
LGNNSTNST	13564	NKTLGNNSTNSTLGN	12908					
VISTRTHRE	13565	ARPVISTRTHREKKA	12909					
WRWGTFLG	13566	QNLWRWGTFLGMLM	12910					
WRWGTMLLG	13567	QHILWRWGTMLLGMLM	12911					
FAVLSIVNR	13568	RIVFAVLSIVNRVQ	12912					
LLNGSLAE	13569	TQLLLNGSLAEFV	12913					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LTPLCVTLN	13570	CVKLTPLCVTLNCTD	12914								
LYKYKVVKI	13571	RSELYKYKVVKIEPL	12915								
VPWNSSWSN	13572	TTNVPWNSSWSNKS	12916	0.0066	0.0320	0.0014		0.0011	0.0190	0.0042	
YRLINCNTS	13573	YKEYRLINCNTSAIT	12917								
IHYCAPAGF	13574	PIPIHYCAPAGFAIL	12918								
LKDQQLGI	13575	ERYLKDQQLGIWGC	12919								
YKYKVVKIE	13576	SELYKYKVVKIEPLG	12920								
IRPVSTQL	13577	THGIRPVSTQLLLN	12921								
LDKWASLWN	13578	LLALDKWASLWNWFD	12922								
LRIVFAVLS	13579	LIGLRIVFAVLSVN	12923								
LNGLAEVE	13580	QLLLNGLAEVEVI	12924								
YKVVKIEPL	13581	LYKYKVVKIEPLGVA	12925								
LKGLRLGWE	13582	RSSLKGLRLGWEGLK	12926								
FSYHRLRDL	13583	LCLFSYHRLRDLILI	12927								
INCTRPNN	13584	SVEINCTRPNNTRK	12928								
VVKIEPLGV	13585	KYKVVKIEPLGVAPT	12929								
WKEATTLF	13586	VPVWKEATTLFCAS	12930	0.0260	-0.0002	0.0520	-0.0030	0.1100	0.0900	0.0021	-0.0045
IGLRIVFAV	13587	GGLIGLRIVFAVLSI	12931								
FFYCNTSGL	13588	GGEFFYCNTSGLFNS	12932								
FGLGALFLG	13589	RAAFGLGALFLGFLG	12933								
FYCNTSGLF	13590	GEFFYCNTSGLFNST	12934								
LIGLRIVFA	13591	VGGLIGLRIVFAVLS	12935								
VGLGAVFLG	13592	KRAVGLGAVFLGFLG	12936								
ICTTAVPWN	13593	KRAVGLGMLFLGVLS	12937								
ICTTAVPWN	13594	GKLICTTAVPWNSSW	12938								
LGVAPTKAK	13595	GKLICTTAVPWNSSW	12939								
LICTTAVPW	13596	IEPLGVAPTAKARRV	12940								
LRDQQLGI	13597	SGKLICTTAVPWNSS	12941								
VFLGFLGAA	13598	ERYLRDQQLGIWGC	12942								
FSYHRLRDF	13599	LGAVFLGFLGAAAGST	12943								
IPHYCTPA	13600	LCLFSYHRLRDFILI	12944								
IVFAVLSIV	13601	FEPIPHYCTPAGFA	12945								
VFAVLSIVN	13602	GLRIVFAVLSIVNRV	12946								
VPWNASWSN	13603	LRIVFAVLSIVNRVR	12947								
IGLRIVFAV	13604	TTAVPWNASWSNKS	12948								
IRQAHCNIS	13605	GGLIGLRIVFAVLSI	12949								
VAPTAKARR	13606	IGDIRQAHCNISRAK	12950								
FNGTGPCKN	13607	PLGVAPTAKARRVVQ	12951								
IGPGQTFYA	13608	DKKFNGTGPCKNVST	12952								
IGSGQAFYV	13609	SVRIGPGQTFYATGD	12953								
IRYLNLVNQ	13610	RYSIGSGQAFYVTGK	12954								
LIGLRIFA	13611	QTAIRYLNLVNQTEN	12955								
LLOYWSQEL	13612	VGGLIGLRIFAVLS	12956								
LRNLCLFSY	13613	WWNLLOYWSQELKNS	12957								
LVSGFLALA	13614	WDDLRLNCLFSYHRL	12958								
VSGFLALAW	13615	SIRLVSGFLALAWDD	12959								
FDPIPHYC	13616	IRLVSGFLALAWDDL	12960								
IFFAVLSIV	13617	KVTFDPIPHYCTPA	12961								
LINCNTSAI	13618	GLRIFAFAVLSIVNRV	12962								
	13619	EYRLINCNTSAITQA	12963								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LTPLCVTLN	13570	CVKLTPLCVTLNCTD	12914					
LYKYKVVKI	13571	RSELYKYKVVKIEPL	12915					
VPWNSSWSN	13572	TTNVPNSSWSNKSLS	12916					
YRLNCTS	13573	YREYRLNCTNSAIT	12917					
IHYCAPAGF	13574	PIPHYCAPAGFAIL	12918					
LKDOQLLGI	13575	ERYLKDOQLLGIWGC	12919					
YKYKVVKIE	13576	SELYKYKVVKIEPLG	12920					
IRPVVSTQL	13577	THGIRPVVSTQLLN	12921					
LDKWSLWN	13578	LLALDKWSLWNWFD	12922					
LRVFAVLS	13579	LIGLRVFAVLSIVN	12923					
LNGLAEFE	13580	QLLLNGSLAEFEVVI	12924					
YKVVKIEPL	13581	LYKYKVVKIEPLGVA	12925					
LKGLRLGWE	13582	RSLKGLRLGWEGLK	12926					
FSYHRLRDL	13583	LCLFSYHRLRLDLLI	12927					
INCTRPNN	13584	SYEINCTRPNNIRK	12928					
VVKIEPLGV	13585	KYKVVKIEPLGVAPT	12929					
WKEATTTLF	13586	VPVWKEATTTLF-CAS	12930	0.0004	0.0630	0.0086	0.4700	
IGLRVFAV	13587	GGLIGLRVFAVLSI	12931					
FFYCNTSGL	13588	GGEFFYCNTSGLFNS	12932					
FGLGALFLG	13589	RAAFGLGALFLGFLG	12933					
FYCNTSGLF	13590	GGEFFYCNTSGLFNST	12934					
LIGLRVFA	13591	VGGIGLRVFAVLS	12935					
VGLGAVFLG	13592	KKAVGLGAVFLGFLG	12936					
VGLGMLFLG	13593	KKAVGLGMLFLGVLS	12937					
ICTTAVPNW	13594	GKLICTTAVPNSSW	12938					
ICTTNVPWN	13595	GKLICTTNVPWNSSW	12939					
LGVAPTAK	13596	IEPLGVAPTAKRRV	12940					
LICTTAVPW	13597	SOKLICTTAVPNSS	12941					
LRDQQLGI	13598	ERYLRDQQLGIWGC	12942					
VFLGFLGAA	13599	LGAVFLGFLGAAAGST	12943					
FSYHRLRDF	13600	LCLFSYHRLRDFLI	12944					
IPHYCTPA	13601	FEPIPHYCTIPAGFA	12945					
VFVAVLSIV	13602	GLRVFAVLSIVNRV	12946					
VPWNASWSN	13603	LRVFAVLSIVNRVR	12947					
IGLRVFAV	13605	TTAVPNASWSNKSLS	12948					
IRQAHCNIS	13606	GGLIGLRVFAVLSI	12949					
VAPTAKRR	13607	IGDIKQAHCNISRAK	12950					
FNGTGPCKN	13608	PLGVAPTAKRRVVQ	12951					
IGPGQIFYA	13609	DKKFNGTGPCKNVST	12952					
IGSQAFYV	13610	SVRIGPGQIFYATGD	12953					
IRYLNLVNQ	13611	RYSIGSQAFYVTGK	12954					
LLQYWSQEL	13612	QIAIRYLNLVNQIEN	12955					
LRNLCLEFY	13614	VGGLIGLRVFAVLS	12956					
LVSGFLALA	13615	WNLLQYWSQELKNS	12957					
VSGFLALAW	13616	WDDLRLNLCLEFYHRL	12958					
FDPIPIHYC	13617	SIRLVSGFLALAWDDL	12959					
IIFAVLSIV	13618	IRLVSGFLALAWDDL	12960					
LINCNTSAI	13619	KVTFDPIPIHYCTPA	12961					
		GLRIIFAVLSIVNRV	12962					
		EYRLINCNTSAITQA	12963					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wB1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LLNATAIAV	13620	AVSLNATAIAVAEG	12964								
LRIIFAVLS	13621	LIGLRIIFAVLSVN	12965								
VITQACPKV	13622	NTSVITQACPKVSFE	12966								
YWNLLQYW	13623	VLKYWNLLQYWSQE	12967								
FAILKCNK	13624	PAGFAILKCNKKFN	12968								
IFAVLSVN	13625	LRIIFAVLSVNRVR	12969								
INCNTSAIT	13626	YRLINCNTSAITQAC	12970								
LNATAIAVA	13627	VSLNATAIAVAEGT	12971								
WNSSWSNKS	13628	NVPWNSSWSNKSLE	12972								
WNASWSNKS	13629	NVPWNASWSNKSIED	12973								
ICTTTPWN	13630	GKLICTTTPWNASW	12974								
LLKLTWGI	13631	QQHLLKLTWGIKQL	12975								
LYKYKVEI	13632	RSELYKYKVEIKPL	12976								
MFLGFLGAA	13633	LGAMFLGFLGAAST	12977								
MHSFNCGGE	13634	EIVMHSFNCGGEFFY	12978								
YWSQELKNS	13635	LLQYWSQELKNSAVS	12979								
IGAVFLGFL	13636	AVGIGAVFLGFLGAA	12980								
LIAARTVEL	13637	DFLIAARTVELLGH	12981								
LICTTTPW	13638	SGKLICTTTPWPNAS	12982								
LNGLSLAEG	13639	TQLLNGSLAEGEII	12983								
YWGQELKNS	13640	LVWYWGQELKNSAIS	12984								
IAARTVELL	13641	FILIAARTVELLGHIS	12985								
LFLGFLGAA	13642	IGALFLGFLGAAST	12986								
LKNSAVSL	13643	SQELKNSAVSLNAT	12987								
VGIGAVFLG	13644	KRAVGIGAVFLGFLG	12988								
VSLNATAI	13645	NSAVSLNATAIAVA	12989								
YATGDIGD	13646	QTFYATGDIGDIRQ	12990								
IAIAVAEGT	13647	LDIIAIAVAEGTDRI	12991								
IHYCTPAGF	13648	PIPIHYCTPAGFAIL	12992								
ILGLVIICS	13649	GTLILGLVIICSASN	12993								
IWNMTWME	13650	VDEIWNMTWMEWER	12994								
LGLVIICSA	13651	TLILGLVIICSASN	12995								
LRDFILIAA	13652	YHRLRDFILIAARTV	12996								
LTPLCVTL	13653	CVKLTPLCVTLDCN	12997								
MLQLTVWGI	13654	QQHMLQLTVWGIKQL	12998								
VEINCTRN	13655	NESVEINCTRNNT	12999								
VRQLLSGIV	13656	TVQVRQLLSGIVQQ	13000								
LILGLVIIC	13657	WGTLILGLVIICSAS	13001								
VGGHQAAMQ	13658	LNTVGGHQAAMQMLK	13002								
LLVQNANPD	13659	TETLLVQNANPDCKT	13003								
VQNANPDK	13660	TLLVQNANPDCKTIL	13004								
LGLNKIVRM	13661	WILGLNKIVRMYS	13005								
LSEGATPD	13662	FSALSEGATPDQNT	13006								
WILGLNKI	13663	YKRWILGLNKIVRM	13007								
LEEMMTACQ	13664	GATLEEMMTACQGVG	13008								
YKRWIILGL	13665	GEIYKRWIILGLNKI	13009								
IYKRWIILG	13666	VGEIYKRWIILGLNK	13010								
VSONYPIVQ	13667	SSQVSONYPIVQNLQ	13011								
WEKIRLRPG	13668	LDKWEKIRLRPGKK	13012								
IAGTSTLQ	13669	GSDIAGTSTLQEQI	13013								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LLNATAIAV	13620	AVSLNATAIAVAEG	12964					
LRIFAVLS	13621	LIGLRIFAVLSVN	12965					
VITQACPKV	13622	NTSVITQACPKVSPE	12966					
YWWNLLQYW	13623	VLKSYWWNLLQYWSQE	12967					
FAILKCNDK	13624	PAGFAILKCNDDKEN	12968					
IFAVLSVN	13625	LRIFAVLSVNVK	12969					
INCNTSAIT	13626	YRLINCNTSAITQAC	12970					
LNATAIAVA	13627	VSLNATAIAVAEGT	12971					
WNSSWSNKS	13628	NVPWNSSWSNKSLE	12972					
WNASWSNKS	13629	NVPWNASWSNKSIED	12973					
ICTTTPWN	13630	GKLCICTTTPWNASW	12974					
LLKLTWGI	13631	QQHLLKLTWGIKQL	12975					
LYKYKVEI	13632	RSELYKYKVEIKPL	12976					
MFLGFLGAA	13633	LGAMFLGFLGAAAGST	12977					
MIISFNCGE	13634	EIVMISHFNCGEFFY	12978					
YWSQELKNS	13635	LLQYWSQELKNSAVS	12979					
IGAVFLGFL	13636	AVGIGAVFLGFLGAA	12980					
LIAARTVEL	13637	DHIAARTVELLGH	12981					
LICTTTPWP	13638	IQLLNGSLAEGEII	12982					
LLNGSLAEG	13639	LVWYWGQELKNSAIS	12983					
YWGQELKNS	13640	FILIAARTVELLGH	12984					
IAARTVELL	13641	IGALFLGFLGAAAGST	12985					
FLGFLGAA	13642	SOELKNSAVSLNAT	12986					
LKNSAVSL	13643	KRAVGIGAVFLGFLG	12987					
VGIGAVFLG	13644	NSAVSLNATAIAVA	12988					
VSLNATAI	13645	QTFYATIGDIGDIRQ	12989					
YATGDIGD	13646	LDIAIAVAEGTDRI	12990					
IAIAVAEGT	13647	PIPIHYCTIPAGFAIL	12991					
IHYCTPAGF	13648	GTLILGLVICSASN	12992					
ILGLVICS	13649	VDEIWNMTWMEWER	12993					
IWNMTWME	13650	TLLGLVICSASN	12994					
LGLVICS	13651	YHRLKDFILIAARTV	12995					
LRDFILIA	13652	CVKLTPLCVTLICHN	12996					
LTPLCVTLD	13653	QQHMLQLTVWGIKQL	12997					
MLQLTVWGI	13654	NEVSEINCIRPNNT	12998					
VEINCTRPN	13655	IYQVVRQLLSGIVQQ	12999					
VRQLLSGIV	13656	WGTLILGLVICSAS	13000					
LILGLVICS	13657	LNTVGGHQAAAMQMLK	13001					
VGGHQAAAMQ	13658	TEILLVQNANPDCKT	13002					
LLVQNANPD	13659	TLLVQNANPDCKTIL	13003					
VQNANPDCK	13660	WILLGLNKVIRMYSP	13004					
LGLNKVIR	13661	FSALSSEATPQDLNT	13005					
LSEGATPDQ	13662	YKRWILGLNKIVRM	13006					
WILGLNKI	13663	GATLEMMIACQGVG	13007					
LEEMMTACQ	13664	GEIYKRWILGLNKI	13008					
YKRWILGL	13665	SSQVSYNTIVQNLQ	13009					
IYKRWILG	13666	VGEIYKRWILGLNK	13010					
VSONYPIVQ	13667	LDKWEKIRLPGGKK	13011					
WEKIRLPG	13668	GSDIAGITSTLQEQI	13012					
IAGTTSTLQ	13669		13013					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w6l	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
WASKELERF	13670	HLVWASRELERFALN	13014								
IPMFALSE	13671	PEVPMFALSSEGAT	13015								
MFALSSEGA	13672	VIPMFALSSEGA TPQ	13016	0.0085		-0.0014		0.0058		-0.0010	
VIPMFALS	13673	SPEVPMFALSSEGA	13017	0.0460	0.0280	0.0034	-0.0043	0.1600		0.0075	-0.0045
MYSPVSILD	13674	IVRMYSPPVSILDIRQ	13018								
IVRMYSPPVS	13675	LNKIVRMYSPPVSILD	13019								
VRMYSPPVS	13676	NKIVRMYSPPVSILDI	13020								
YSPVSILDI	13677	VRMYSPPVSILDIRQ	13021								
MTETLLVQN	13678	KNWMTETLLVQANP	13022								
WMETLLVQ	13679	VKNWMTETLLVQANV	13023								
ISPRTLNAW	13680	IQAISPRTLNAWVKV	13024								
VKNWMTETL	13681	TOEVKNWMTETLLVQ	13025	0.0033	0.0130	0.0077	-0.0043	0.0480		-0.0010	-0.0045
IKCFNCGKE	13682	QKRKICFNCGKEGHL	13026								
IPVGEIYKR	13683	NPPIPVGEIYKRWII	13027								
YTAVFMQRG	13684	KGGYTAVFMQRGNP	13028								
VATLYCVHQ	13685	YNTVATLYCVHQRIE	13029								
WDRLLIPVIA	13686	AAEWDRLLIPVIA GPI	13030								
FLOSRRPEPT	13687	PGNFLOSRRPEPTAPP	13031	0.0970		0.0170		0.0190		0.0015	
FKTLRAEQA	13688	DRFFKTLRAEQATQE	13032								
MVHQAI SPR	13689	QGMVHQAI SPRTLNA	13033	0.0690	0.1400	1.5000	0.0170	0.8300	0.0950	-0.0010	0.0048
VHQAI SPR	13690	QGMVHQAI SPRTLNA	13034	0.0003		0.0023		0.0034		-0.0010	
YKTLRAEQA	13691	DRFYKTLRAEQASQE	13035	0.0530	0.0016	0.0500		0.1500		0.0430	
VSILDIRQ	13692	YSPVSILDIRQPKKE	13036								
LAEAMSQVT	13693	ARVLAEAMSQVTNSA	13037								
LGIKWPSHK	13694	ANFLGIKWPSHKGRP	13038								
VKCFNCGKE	13695	RKTVKCFNCGKEGHI	13039								
YNTVATLYC	13696	RSLYNTVATLYCVHIQ	13040								
LIPVIA GPI	13697	WDRLLIPVIA GPIAG	13041								
LYNTVATLY	13698	LRSLYNTVATLYCVHI	13042								
MTDTLLVQN	13699	KNWMTDTLLVQANP	13043								
WMTDTLLVQ	13700	VKNWMTDTLLVQANP	13044								
IEVKDTKEA	13701	HQRIEVDKTEALDK	13045								
LOGQMVHQ	13702	VQNLQGMVHQAI SP	13046								
MTNNPPIP	13703	IGWMTNNPPIPVGEI	13047								
WMTNNPPIP	13704	QIGWMTNNPPIPVGE	13048								
IAPGQMRP	13705	AGPIAPGQMRPGRS	13049								
VHAGPIAPG	13706	LHPVHAGPIAPGQMR	13050								
LGPGATLEE	13707	LRALPGATLEEEMMT	13051								
VHAGPIPG	13708	VHPVHAGPIPGQMR	13052								
IPPGQMRP	13709	AGPIPGQMRPGRS	13053								
LSPRTLNAW	13710	HQALSPTLNAWVKV	13054								
YRLKHLVWA	13711	KKKYRLKHLVWASRE	13055								
LGPAATLEE	13712	LKALGPAATLEEEMMT	13056								
LKALGPAAT	13713	KTILKALGPAATLEE	13057	0.0760		0.0100		-0.0023		-0.0010	
LKKEPPLA	13714	QEQLKKEPPLASLR	13058								
LSGKLD AW	13715	ASVLSGGKLD AWKEI	13059								
MTSNPPIP	13716	IGWMTSNPPIPVGEI	13060								
VKNWMTDTL	13717	TQDVKNWMTDTLLVQ	13061								
VSILDIKOG	13718	YSPVSILDIKOGPKKE	13062								
WMTSNPPIP	13719	QIGWMTSNPPIPVGE	13063								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
WASRELERF	13670	HLVWASRELERFALN	13014					
IPMFSALE	13671	PEVPMFSALSEGAT	13015					
MFSALEGA	13672	VIPMFSALEGAIPQ	13016					
VIPMFSALE	13673	SPEVPMFSALSEGAT	13017	0.0007	-0.0007	0.0130	0.0130	
MYSVPSILD	13674	IVRMYSVPSILDIRQ	13018					
IVRMYSVPS	13675	LNKIVRMYSVPSILD	13019					
VRMYSVPSI	13676	NRMYSPVPSILDI	13020					
YSPVSILDI	13677	VRMYSVPSILDIRQ	13021					
MTETLLVQN	13678	KNWMTETLLVQNANP	13022					
WMTETLLVQ	13679	VKNWMTETLLVQNAN	13023					
ISPRTLNAW	13680	HQAISPRTLNAWVKV	13024					
VKNWMTETL	13681	TQEVKNWMTETLLVQ	13025	0.0032	0.0280	0.0008	0.0053	
IKCFNCCKE	13682	QKRKCTNCGKEGHL	13026					
IPVGEIYKR	13683	NPPPVGEIYKRWII	13027					
YTAVFMRQ	13684	KGGYIAVFMQRGQNP	13028					
VATLYCVHQ	13685	YNIVATLYCVHQRIE	13029					
WDRLLIPVIA	13686	AAEWDRLLIPVHAGPI	13030					
FLQSRPEPT	13687	PGNPLQSRPEPTAPP	13031		0.0130			
FKTLRAEQ	13688	DRFKTLRAEQATQE	13032					
MVHQASPR	13689	QGMVHQASPRILN	13033	0.0085	0.0550	0.0067	-0.6400	
VHQASPR	13690	GQMVHQASPRILNA	13034					
YKTLRAEQ	13691	DRFYKTLRAEQASQE	13035	-0.0001	-0.0007		-0.0015	
VSILDIRQ	13692	YSPVSILDIRQPKKE	13036		0.0028			
LAEAMSVQT	13693	ARVLAEAMSVQVINS	13037					
LKGIWPSHK	13694	ANFLGKIWPFSKGRIP	13038					
VKCFNCCKE	13695	RKIVKCFNCCKEGHI	13039					
YNIVATLYC	13696	RSLYNIVATLYCVHQ	13040					
LHPVHAGPI	13697	WDRLLIPVHAGPIAG	13041					
LYNTVATLY	13698	LKSLYNIVATLYCVH	13042					
MTDTLLVQN	13699	KNWMTDTLLVQNANP	13043					
WMTDTLLVQ	13700	VKNWMTDTLLVQNAN	13044					
IEVKDTKEA	13701	HQRIEVKDTKEALDK	13045					
LOGQMVHQ	13702	VQNLQGMVHQASIP	13046					
MTNNPIPV	13703	IGWMTNNPIPVGEI	13047					
WMTNNPIPV	13704	QIGWMTNNPIPVGE	13048					
IAPQGMREP	13705	AGPIAPQGMREPGRS	13049					
VHAGPIAPG	13706	LHPVHAGPIAPGQMR	13050					
LGPATLEE	13707	LKALGPAATLEEEMI	13051					
VHAGPIPPG	13708	VHPVHAGPIPPGQMR	13052					
IPPGQMRREP	13709	AGPIPPGQMRREPGRS	13053					
LSPRTLNAW	13710	HQAISPRTLNAWVKV	13054					
YRLKILVVA	13711	KKKYRLKILVWASRE	13055					
LGPATLEE	13712	LKALGPAATLEEEMI	13056		0.0006			
LKALGPAAT	13713	KIILKALGPAATLEE	13057					
LKDKEPPLA	13714	QEQLKDKEPPLASLR	13058					
LSGGKLDW	13715	ASVLSGGKLDWAWKI	13059					
MTSNPIPV	13716	IGWMTSNPIPVGEI	13060					
VKNWMTDTL	13717	TQDVKNWMTDTLLVQ	13061					
VSILDIRQ	13718	YSPVSILDIRQPKKE	13062					
WMTSNPIPV	13719	QIGWMTSNPIPVGE	13063					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wB1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
ENTVATLYC	13720	KSLFNTVATLYCVHQ	13064								
IPMFTALSE	13721	PEVIPMFTALSEGAT	13065								
LASLSLFG	13722	LYPLASLSLSLFGNDP	13066								
LERFAVNP	13723	SRELERFAVNPGLLE	13067								
LFNTVATLY	13724	LRSLFNTVATLYCVH	13068								
MFALSEGA	13725	VIPMFTALSEGATPQ	13069								
WDRVHPVHA	13726	AAEWDRVHPVHAGPI	13070								
IVRMYSPTS	13727	LNKIVRMYSPTSILD	13071								
LERFALNPG	13728	SRELERFALNPGLE	13072								
LOEQIAWMT	13729	TSTLOEQIAWMTGNP	13073								
VIIPVHAGPI	13730	WDRVIIPVHAGPIPG	13074								
VIPMFTALS	13731	SPEVIPMFTALSEGA	13075								
VRMYSPTS	13732	NKIVRMYSPTSILDI	13076								
LCKIWPSNK	13733	ANFLGKIWPSNKGPR	13077								
LTSLSLFG	13734	LYPLTSLKSLFGNDP	13078								
MYSPSILD	13735	IVRMYSPTSILDIRQ	13079								
YKLHIVWA	13736	KKKYKLHIVWASRE	13080								
YSPSILDI	13737	VRMYSPTSILDIRQ	13081								
LTSLSLFG	13738	LYPLTSLRSLFGNDP	13082								
MLNIVGGH	13739	DLNMLNIVGGHQA	13083								
IDVKDTKEA	13740	HQRIDVKDTKEALDK	13084								
IGWNTSNP	13741	QEQIGWNTSNPIPVP	13085								
IPVGDYKR	13742	NPIPVGDIYKRWII	13086								
LYPLASLS	13743	DKELYPLASLSLFG	13087								
VHQALSPT	13744	GQMVHQALSPTLNA	13088								
VNPGLLETS	13745	REAVNPGLLETS	13089								
YPLASLSL	13746	KELYPLASLSLFGN	13090								
FLQNRPEPT	13747	PGNFLQNRPEPTAPP	13091								
IMMOKSNFK	13748	AAAIMMOKSNFKGPR	13092								
LAEAMSQVQ	13749	ARVLAEAMSQVQSQN	13093								
LCKIWPSK	13750	ANFLGKIWPSKGRP	13094								
LNPGLLETA	13751	REALNPGLLETAEGC	13095								
YPLASLSL	13752	KELYPLASLSLFGN	13096								
WQNYTPGPG	13753	FPDWQNYTPGPGIRY	13097								
VRPQVPLRP	13754	GFPRPQVPLRPMTY	13098								
VPLRPMYK	13755	RPQVPLRPMYKGA	13099								
LTFGWCFKL	13756	RYPLTFGWCFKLVPV	13100								
ILDWVYHT	13757	RQELDLWVYHTQGY	13101								
WCFKLVPVD	13758	TFGWCFKLVPVDPRE	13102								
LWYHTQGY	13759	ILDLWVYHTQGYFPD	13103								
WSKSSIVGW	13760	GGKWSKSSIVGWPAI	13104								
ILDWVYNT	13761	RQDILDWVYNTQGY	13105								
LLHPMSQHG	13762	NNCLLHPMSQHGMD	13106								
LLHPICQHG	13763	NNLLHPICQHGMD	13107								
IRYPLTFGW	13764	PGIRYPLTFGWCFK	13108								
ITSSNTAAT	13765	HGAITSNTAATNAD	13109								
LEKHGATIS	13766	SRDLEKHGATISNT	13110								
LWVYHTQGF	13767	ILDWVYHTQGFDP	13111								
MTYKGAIDL	13768	LRPMYKGAIDLSPF	13112								
LVPVDPREV	13769	CFKLVPVDPREVEEA	13113								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FNTVATLYC	13720	KSLFNTVATLYCVIIQ	13064					
IPMFTALSE	13721	PEVIPMFTALSEGAT	13065					
LASLSLFG	13722	LYPLASLSKSLFGNDIP	13066					
LERFAVNP	13723	SKELEKFAVNPGLLE	13067					
LFTVATLY	13724	LKSLFNTVATLYCVH	13068					
MFTALSEGA	13725	VIPMFTALSEGATPQ	13069					
WDRVHIPVIA	13726	AAEWDRVHIPVHAGPI	13070					
IVRMYSPTS	13727	LNKIVRMYSPTSILD	13071					
LEREALNPG	13728	SKELEKFAVNPGLLE	13072					
LOEQIAWMT	13729	ISILQEQIAWMTGNP	13073					
VHPVHAGPI	13730	WDRVHIPVHAGPIPG	13074					
VIPMFTALS	13731	SPEVIPMFTALSEGA	13075					
VRMYSPTS	13732	NKIVRMYSPTSILDI	13076					
LKGIWPSNK	13733	ANFLGKIWPSNKGPR	13077					
LTSLSLFG	13734	LYPLTSLSKSLFGNDIP	13078					
MYSPTSILD	13735	IVRMYSPTSILDIRQ	13079					
YKLGHIWA	13736	KKKYKLKHIVWASRE	13080					
YSPTSILDI	13737	VRMYSPTSILDIRQG	13081					
LTSLSLFG	13738	LYPLTSLSKSLFGNDIP	13082					
MMLNIVGGH	13739	DLMMLNIVGGHQA	13083					
IDVKDTKEA	13740	HQRIDVKDTKEALDK	13084					
IGWMTSNIP	13741	QEQIGWMTSNPIPV	13085					
IPVGDIYKR	13742	NPPIPVGDIYKRWII	13086					
LYPLASLS	13743	DKELYPLASLSLFG	13087					
VHQALSPT	13744	GQMVHQALSPTLNA	13088					
VNPGLLETS	13745	REAVNPGLLETSEGC	13089					
YPLASLSL	13746	KELYPLASLSLFGN	13090					
FLQNRPEPT	13747	PGNFLQNRPEPTAPP	13091					
IMMQSNFK	13748	AAAIMMQSNFKGPR	13092					
LAEAMSQVQ	13749	ARVLAEMSQVQSQSN	13093					
LKGIWPSKK	13750	ANFLGKIWPSKKGRP	13094					
LNPGLLETA	13751	REFALNPGLLETAEGC	13095					
YPLASLSL	13752	KELYPLASLSLFGN	13096					
WQNYTPGPG	13753	FPDWQNYTPGPGIRY	13097					
VRPQVPLRP	13754	GFPPVRPQVPLRPMY	13098					
VPLRPMYK	13755	RPQVPLRPMYKGAFF	13099					
LTFGWCFKL	13756	RQELDLWVYHIQGY	13100					
ILDWVYHT	13757	IFGWCFKLVPDPRE	13101					
WCFKLVPVD	13758	ILDLWVYHIQGYEFPD	13102					
LWVYHIQGY	13759	GGKWSKSSIVGWPAI	13103					
WSKSSIVGW	13760	RODILDLWVYHIQGY	13104					
ILDWVYNT	13761	NNCLLHPMSQHGMDD	13105					
LLHPMSQHIG	13762	NNLLHPMSQHGMED	13106					
LLHPICQHIG	13763	GPGRYPLTFGWCFK	13107					
IRYPLTFGW	13764	HGATSSNTAATNAD	13108					
ITSSNTAAT	13765	SRDLKKGATSSNT	13109					
LEKHGATIS	13766	ILDLWVYHIQGYEFPD	13110					
LWVYHIQGY	13767	LRPMYKGAFFDLSFF	13111					
MTYKGAFFDL	13768	CFKLVPDPREVEEA	13112					
LVPDPREVE	13769		13113					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wB1	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VGWPAIRER	13770	SSIVGWPAIRERMRR	13114								
WCFKLPVE	13771	TFGWCFKLPVPEPK	13115								
FDSRLAFHII	13772	EWRFDSRLAFHIIVAR	13116								
FKLVPDPR	13773	GWCFKLPVDPDPREVE	13117								
VPLRPMTFK	13774	RPQVPLRPMTFKGAF	13118								
LLDTGADDT	13775	KEALLDTGADDTVLE	13119	0.0001	-0.0015			-0.0023		-0.0010	
WMGYELIIPD	13776	PFLWMGYELIIPDKWT	13120								
YQYNVLPQG	13777	GIRYQYNVLPQGWKG	13121								
FRKYTAFTI	13778	DKDFRKYTAFTIPSI	13122	0.0027	-0.0014			-0.0026		0.1200	
WTVNDIQKL	13779	KDSWTVNDIQKLVGK	13123								
LDCTHLEK	13780	IWQLDCTHLEKHL	13124					-0.0026		-0.0007	
LDVGDAVES	13781	VTVLVDVGDAVESVPL	13125	0.0003	-0.0014			0.0036		-0.0006	
MDDLYVGS	13782	YQYMDLLYVGSLEI	13126	0.0006	-0.0014		-0.0160				
VPAETGQE	13783	EAEVPAETGQETAY	13127								
WKEGAVVI	13784	KLLWKGEAVVIQDN	13128	0.4600	0.0011	0.0058	-0.0043	0.0750	0.0200	0.0060	-0.0045
WQLDCTHLE	13785	PGIWQLDCTHLEGI	13129								
VDFRELNR	13786	RKLVDFRELNRKTQD	13130								
WPKMIGGI	13787	PGKWKPKMIGGIGF	13131	0.0013	-0.0021			0.0990		-0.0006	
IWQLDCTHIL	13788	SPGIWQLDCTHILEGK	13132								
VAVIVASGY	13789	ILVAVIVASGYIEA	13133					-0.0026		-0.0007	
WKGSPAIQ	13790	PQGWKGSPIAQSSM	13134	0.0010	-0.0014						
IGYSAGER	13791	KGGIGGYSAGERIID	13135								
YALGHIAQ	13792	DSQYALGHIAQAPDK	13136								
FWEVQLGIP	13793	TQDFEWEVQLGIPHPA	13137								
IKKDKSTKW	13794	VFAIKKDKSTKWRL	13138								
LGHQAOPD	13795	QYALGHQAOPDKSE	13139								
LGHIPAGL	13796	EVQLGHIPAGLKKK	13140	0.0020	0.1300	0.1300	0.0220	-0.0026	1.9000	-0.0007	0.2200
VNTPLVLK	13797	WEFVNTPLVLKLWYQ	13141	0.6900	0.0410	9.5000		1.8000		0.0630	
VTVLVGDGA	13798	KKSVTVLVDVGDAYES	13142	0.0019	-0.0014	-0.0014	0.0065	0.0065		0.0030	
FPISPIETV	13799	TLNFPISPIETVPVK	13143	0.0190	0.0003	-0.0014	-0.0043	0.0350	0.0095	-0.0007	0.0370
ISPIETVPV	13800	NFPISPIETVPVKLK	13144	0.0480	0.0013	0.0022	-0.0043	0.0810		-0.0007	0.0460
FVNTPLVK	13801	EWEFVNTPLVKLWY	13145								
LNFPISPIE	13802	GCTLNFPISPIETVP	13146	0.0014	-0.0014	-0.0014	0.0920	-0.0026	1.6000	-0.0006	0.0540
WEFVNTPL	13803	IPWEFVNTPLVKL	13147	1.1000	0.0089	1.8000		0.6600		0.0830	
IQNFRVYR	13804	ITKIQNFRVYRDSR	13148								
LVGTPVNI	13805	GTVLVGTPVNIIGR	13149	0.0066	0.0061	-0.0014	-0.0043	-0.0026		0.0043	-0.0045
VQLGIPHPA	13806	FWEVQLGIPHPAGLK	13150	0.0240		-0.0014		0.0033		-0.0006	
WQATWIPFW	13807	TEYWQATWIPWEFV	13151								
IETVPVKK	13808	ISPIETVPVKLPGM	13152	0.0019	0.0140	0.0140		-0.0026		-0.0007	
IGTVLVGPT	13809	KKAIGTVLVGPTPVN	13153								
LVAVIVASG	13810	KIILVAVIVASGYIE	13154								
VLVGTPVN	13811	IGTVLVGTPVNIIG	13155	0.0120	0.0170	-0.0003		0.0008	0.0030	-0.0004	
YIEAEVIPA	13812	ASGYIEAEVIPAETG	13156	0.0230	-0.0003	-0.0021	-0.0043	0.2300		0.0020	-0.0045
YVGSDELIG	13813	DDLTVGSDELIGQHR	13157								
MDGPKVKQW	13814	KPGMDGPKVKQWPLT	13158								
VASGYIEAE	13815	AVHVASGYIEAEVIP	13159								
VGTPVNI	13816	TVLVGTPVNIIGRN	13160	0.0010	-0.0014			-0.0026		0.0035	
VKQWPLTEE	13817	GPKVQWPLTEEKIK	13161								
VYRDSRDP	13818	NFRVYRDSRDPWK	13162								
WGFTTPDKK	13819	LLRWGFTTPDKKHQK	13163								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VGWPAIRER	13770	SSIVGWPAIRERMRR	13114					
WCFKLVPVE	13771	TFGWCTKLVPEPEK	13115					
FDSRLAFHH	13772	EWRFDSRLAFHHVAR	13116					
FKLVVDPR	13773	GWCTKLVVDPREVE	13117					
VPLRPNTFK	13774	RPQVPLRPMTFKGAF	13118					
LLDTGADDT	13775	KEALLDIGADDIVLE	13119		-0.0003			
WNGYELHPD	13776	PLFWMGYELHPDKWT	13120					
YOYNVLPQG	13777	GIRYOYNVLPQGWKG	13121					
FRKYTAFTI	13778	DKDFRKYTAFIIPSI	13122		-0.0005			
WTVNDIQKL	13779	KDSWTVNDIQKLVGK	13123					
LDCTHLEGG	13780	IWQLDCTHLEGGIIL	13124					
LDVGDAYES	13781	VTVLDVGDAYESVPL	13125		-0.0005			
MDDLYVGSD	13782	YOYMDLLYVGSLLFI	13126		-0.0005			
VIPAETGQE	13783	EAEVIPAETGQETAY	13127					
WKGEGAVVI	13784	KLLWKKGEGAVVIQDN	13128					
WQLDCTHLE	13785	PGIWLDCCTHLEGGI	13129					
VDFRELNKR	13786	RKLVDFRELNKRITQD	13130					
WPKMIGGI	13787	PGKWKPKMIGGIGGF	13131					
IWQLDCTHIL	13788	SPGIWQLDCTHLEGG	13132		-0.0009			
VAVIVASGY	13789	IILVAVHVIVASGYIEA	13133					
WKGSPAIFQ	13790	PQGWKKGSPAIFQSSM	13134		0.0087			
IGGYSAGER	13791	KGGHGGYSAGERIID	13135					
YALGHQAQ	13792	DSQYALGHQAQPDK	13136					
FWEVQLGIP	13793	TQDFWEVQLGIPHPA	13137					
IKKKSTKW	13794	QYALGHQAQPDKSE	13138					
LGHQAQPD	13795	EYQLGHQAQPDKSKK	13139					
LGPIHPAGL	13796	WEEVNIIPPLVKLWYQ	13140					
VNTPLPLVK	13797	KKSVTVLDVGDAYS	13141	0.0390	-0.0005	0.1400	1.9000	
VTVLDVGDA	13798	TLNFPISPIETVPVK	13142		-0.0005	-0.0005	0.0016	
FPISPIETV	13799	NFPISPIETVPVKL	13143	0.0150	0.0640	0.0008	0.0046	
ISPIETVPV	13800	FEWVNTPLPLVKLWY	13144	0.0190	0.1500			
FVNTPLPLV	13801	GC TLNFPISPIETVP	13145		0.0380			
LNFPISPIE	13802	IPFEWVNTPLPLVKL	13146		1.4000	0.2600	2.6000	
WEFVNTPL	13803	ITKQNFVYVYRDSR	13147					
IQNFRVYR	13804	GTVLVGPFPVNIIGR	13148		0.0820		0.0180	
LVGPTPVNI	13805	FWEVQLGIPHPAGLK	13149	0.0290	0.0024	-0.0005		
VQLGIPHPA	13806	TEYWQATWIPEWFEV	13150					
WQATWIPEW	13807	ISPIETVPVKLPGM	13151		0.0150			
IETVPVKLK	13808	KKAGITVLVGPFPVN	13152					
IGTVLVGPT	13809	KIILVAVHVIVASGYIE	13153					
LVAVHVIVASG	13810	IGTVLVGPTPVNIIG	13154					
VLVGPFPVN	13811	ASGYIEAEVIPAETG	13155		0.0710	-0.0003	0.0320	
YIEAEVIPA	13812	DDLYVGSDEIGQHIL	13156	0.0006	0.0120	0.0097	0.0480	
YVGSDEIG	13813	KPGMDGPKVKQWPLI	13157					
MDGPKVKQW	13814	AVHVIVASGYIEAEVIP	13158					
VASGYIEAE	13815	IVLVGPTPVNIIGRN	13159					
VGPTPVNI	13816	GPVKVQWPLTEEKIK	13160					
VKQWPLTEE	13817	NFRVYRDSRDPWK	13161					
VYVYRDSRP	13818	LLRWGFTIPDKKHQK	13162					
WGFTTPDKK	13819		13163					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VIVQYMDL	13820	PEVIYQYMDLLVYG	13164								
LKKKSVTV	13821	PAGLKKKSVTVLVDV	13165	0.0060		-0.0014		-0.0026		-0.0006	
VPRKAKII	13822	IKVVPBRKAKIIRDY	13166	0.0003		0.0700		-0.0024		2.5000	
FPQITLWQR	13823	SFSFTQITLWQRPLV	13167	0.0027				0.0130			
VIWGTTPKF	13824	ESIVIWGTTPKFRPLP	13168								
YVDGAANRE	13825	ETFYVDGAANRETKL	13169								
FNKLKIGKY	13826	QEPFRNLKIGKYAKM	13170								
IOTKELQKQ	13827	ATDIQTKFLOKQITK	13171								
YGKQAGDID	13828	IRDYKQKQAGDIDCA	13172								
WRAMASDFN	13829	ISNWRAMASDFNLP	13173	0.1500	0.0004	0.1600	-0.0030	4.7000	2.6000	0.2100	-0.0045
ISKIGPENP	13830	EGKISKIGPENPYNT	13174								
LTOIGCTLN	13831	RNLLTOIGCTLNPI	13175	0.0001		-0.0014		-0.0026		-0.0007	
IIQAQPKS	13832	ALGHQAQPKSESE	13176								
LPEKDSWTV	13833	PIVLPKDSWTVNDI	13177								
FQSMTKIL	13834	PAIFQSMTKILEPF	13178	0.0320	0.0320	0.0200	-0.0043	0.0058	0.6500	0.0660	-0.0045
FTIPSINNE	13835	YTAFTIPSINNETPG	13179								
IFQSSMTKI	13836	SPAIFQSSMTKILEP	13180	0.0140	0.0420	0.0300	-0.0043	0.0140	0.3500	0.0270	0.0122
IIEQLIKKE	13837	VSQIEQLIKKEKVY	13181								
LSWVPAHKG	13838	KVYLSWVPAHKGIG	13182								
YLSWVPAIK	13839	EKVYLSWVPAIKGIG	13183	0.0270	0.1300	0.0048	-0.0043	0.1700	0.2800	0.0110	0.0089
YTAFTIPSI	13840	FRKYTAFTIPSINNE	13184								
IIATDIQTK	13841	IIIIATDIQTKELQ	13185								
IKKGPAKLL	13842	RDPWKGPAPKLLWK	13186								
LOKQITKIO	13843	TKELQKQITKIQNFR	13187	0.0071	0.0210	0.0350		0.0540	0.0200	0.0530	
LKEALLDTG	13844	GGOLKEALLDTGADD	13188	0.0001		-0.0021		-0.0024		-0.0005	
VYLSWVPAH	13845	KEKVYLSWVPAIKGI	13189								
FILKLAGRW	13846	TAYFILKLAGRWPKV	13190								
LFGKILVA	13847	CTHILEGKILVAVIV	13191								
YFILKLAGR	13848	ETAYFILKLAGRWPV	13192								
ILVAVHVA	13849	EGKILVAVHVASGY	13193								
IWGTTPKFR	13850	SIVIWGKTPKFRPLP	13194								
LAGRWPKV	13851	ILKLAGRWPVKVIHT	13195								
VVAKEIVAS	13852	LPPVVAKEIVASCDK	13196	0.0001		-0.0021		0.0043		-0.0010	
IIIIATDIQ	13853	ERIIIIATDIQITKE	13197								
IIIIATDI	13854	GERIIIIATDIQTK	13198								
IIGRNMLTQ	13855	PVNIIGRNMLTQIGC	13199								
IKVKQLCKL	13856	YAGIKVKQLCKLLRG	13200								
VDKLVSSGI	13857	NEQVDKLVSSGIRKV	13201								
IVGAETFYV	13858	KEPIVGAETFYVDGA	13202								
LPPVVAKEI	13859	DFNLPPVVAKEIVAS	13203	0.0042		-0.0021		-0.0024		0.0036	
WTVQPIQLP	13860	PDKWTVPQIQLPEKD	13204								
FNLPPVAK	13861	ASDFNLPPVVAKEIV	13205	0.0026		-0.0021		-0.0028		-0.0006	
FTSAAVKAA	13862	GSNFTSAAVKAAACWW	13206								
LALQDSGLE	13863	AIHLALQDSGLEVNI	13207								
LPPVVAKEI	13864	DFNLPPVVAKEIVAS	13208								
LQDSGLEVN	13865	HLALQDSGLEVNIVT	13209								
FNLPPVAK	13866	ASDFNLPPVVAKEIV	13210								
IGQHRAKIE	13867	DLEIGQHRAKIEELR	13211								
IGRNLLTQ	13868	PVNIIGRNLLTQIGC	13212	0.0059		-0.0014		0.0043		0.0990	
LEVINVTDS	13869	DSGLEVINVTDSQYA	13213	0.0001		-0.0014		0.0350		-0.0007	

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VYQYMDL	13820	PLVITYQYMDLLVYG	13164					
LKKKSVTV	13821	PAGLKKKSVTVLVDV	13165		0.0140			
VPRKAKII	13822	IKVVPRKAKIIRDY	13166		0.0030			
FPQITLWQR	13823	SFSFPQITLWQRPLV	13167		0.0006			
VIWGTKPKF	13824	ESIVWGTKPKFRLLP	13168					
YVDGAANRE	13825	EIFYVDGAANRETKL	13169					
FKNLKTGY	13826	QEPFKNLKTGYAKM	13170					
IOTKELQKQ	13827	AIDIQTKELQKQTK	13171					
YKQOMAGDD	13828	IRDYKQOMAGDDCVA	13172	0.0008	0.0530	0.0250	0.0860	
WRAMASDFN	13829	HSNWRAMASDFNLPP	13173					
ISKIGPENP	13830	EGKISKIGPENPYNT	13174					
LTQIGCTLN	13831	RNLLTQIGCTLNFPI	13175		-0.0005			
IOAQPKS	13832	ALGHQAQPKSESE	13176					
LPEKDSWTV	13833	PVLPPEKDSWTVNDI	13177					
FQSSMTKIL	13834	PAIFQSSMTKILEPF	13178	0.1100	0.7300	0.0140	0.9100	
FTIPSINNE	13835	YTAFTIPSINNETPG	13179					
IFQSSMTKI	13836	SPAFIFQSSMTKILEP	13180	0.2800	0.3700	0.0150	2.3000	
IEQLIKE	13837	VSQIEQLIKEKIKVY	13181					
LSWVPAHKG	13838	KVYLSWVPAHKGIGG	13182					
YLSWVPAHK	13839	EKVYLSWVPAHKIGG	13183					
YTAFTIPSI	13840	FRKYTAFTIPSINNE	13184	-0.0004	0.8400	0.0610	1.9000	
IIATIDIQIK	13841	IIIDIIATIDIQIKELQ	13185					
IKWGPAKLL	13842	RDPWKGPAKLLWKG	13186					
LQKQTKIQ	13843	TKELQKQTKIQNFR	13187					
LKEALDTG	13844	GGQLKEALDTGADD	13188		0.0055	0.0250	0.0028	
VYLSWVPAH	13845	KEKVYLSWVPAHKGI	13189		-0.0009			
FILKLAGRW	13846	TAYFILKLAGRWPKV	13190					
LEGKILVA	13847	CTHLEGKILVAVHV	13191					
YFILKLAGR	13848	EYAYFILKLAGRWPV	13192					
ILVAVHVA	13849	EGKILVAVHVASGY	13193					
IWGKTPKFR	13850	SIVIWGKTPKFRLLPI	13194					
LAGRWPVKV	13851	ILKLAGRWPVKVIHT	13195					
VVAKEIVAS	13852	LPPVVAKEIVASCDK	13196		-0.0009			
IDIIATDIQ	13853	ERIDIIATIDIQIKE	13197					
IIGRNMLTQ	13854	GERIDIIATIDIQIK	13198					
IKVKQLCKL	13855	PVNIIGRNMLTQIGC	13199					
VDKLVSIGI	13856	YAGIKVKQLCKLLRG	13200					
IVGAETFYV	13857	NEQVDKLVSSGIRKV	13201					
LPPVVAKEI	13858	KEPIVGAETFYVDGA	13202					
WTVQPIQLP	13859	DFNLPPVVAKEIVAS	13203		0.0530			
FNLPPVVAK	13860	PDKWTVQPIQLPEKD	13204					
FTSAAVKAA	13861	ASDFNLPPVVAKEIV	13205		0.0840			
LALQDSGLE	13862	GSNFTSAAVKAAACWW	13206					
LPPVVAKEI	13863	AIHLALQDSGLEVNI	13207					
LQDSGLEVN	13864	DFNLPPVVAKEIVAS	13208					
FNLPPVVAK	13865	HLALQDSGLEVNIVI	13209					
IGQIRAKIE	13866	ASDFNLPPVVAKEIV	13210					
HGRNLLTQ	13867	DLEIGQIRAKIEELR	13211					
LEVNIVTDS	13868	PVNIIGRNLLTQIGC	13212		-0.0005			
	13869	DSGLEVNIVTDSQYA	13213		-0.0005			

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w262	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LRGAKALTD	13870	CKLLRGAKALTDIVP	13214								
LVSSGIRKV	13871	VDKLVSSGIRKVLFL	13215								
FLKLKAGR	13872	TAYFLKLKAGRWPVK	13216								
LALQDSGE	13873	AHILALQDSGSEVNI	13217								
LQDSGSEVN	13874	HLALQDSGSEVNIVT	13218								
VKVIITDNG	13875	RWPVKVIITDNGSNF	13219								
WPKVVIHTD	13876	AGRPVKVIHTDNGS	13220					0.0210			
YFLKLAGR	13877	ETAYFLKLKAGRWPV	13221	0.0610							
ICGKKAIGT	13878	LIEICGKKAIGTVL	13222								
IVAKEIVAS	13879	LPPIVAKEIVASCDK	13223								
LRWGFTHPD	13880	QHLLRWGFTTPDKKH	13224								
LEGKVLVA	13881	CTHLEGKVLVAVHIV	13225								
LKWGFTHPD	13882	EHLKKGFTTPDKKH	13226								
VILVAHVA	13883	EGKVILVAVHVASGY	13227								
LAWVPAHKG	13884	KVYLAWVPAHKGHGG	13228								
YDQILIEIC	13885	VRQYDQILIEICGKK	13229								
IGQIRTKIE	13886	EKVYLAWVPAHKGHGG	13230	0.6000	0.3700	0.8200	0.0049	0.3200	0.2300	0.2800	0.0240
IGRNLITQI	13887	DLEIGQIRTKIEELR	13231								
LWORPLVTI	13888	VNIIGRNLITQIGCT	13232								
VSLTETTNQ	13889	QITLWQRPVLTIGIG	13233								
VYLAWVPAH	13890	OKVVSLETETTNOKTE	13234								
ICGKKAIGT	13891	KEKVYLAWVPAHKGH	13235								
LRGKALTE	13892	LIEICGKKAIGTVLV	13236								
LVNQIEQL	13893	CKLLRGTKALTEVIP	13237								
LVSQIEQL	13895	ESELVSNQIEQLIKK	13238								
YFSVPLDKD	13896	GDAYSFVPLDKDFRK	13240	0.0059		0.0210		0.0095		0.0009	
IKVRQLCKL	13897	VNIIGRNLITQIGCT	13241								
LWGPAPKLL	13898	YPGIKVRQLCKLLRG	13242								
LWQRPVTV	13900	RDPLWGPAPKLLWKG	13243								
YAGIKVKQL	13901	QITLWQRPVLTIGIG	13244								
IWKGTPKFK	13902	SOIYAGIKVKQLCKL	13245								
LRHLKKGW	13903	SIVIWGTGTPKFKLPI	13246								
VQPIQLPEK	13904	IEELREHLKKGWFTT	13247								
WQRPVTK	13905	KWTVQPIQLPEKDSW	13248								
IIOAQPDRS	13906	ITLWQRPVLTIGIG	13249								
LQAHILALQ	13907	ALGIHQAPDRSESE	13250								
LVEICTEME	13908	KTELQAHILALQDSG	13251								
LRQHLLRWG	13909	IKALVEICTEMEKEG	13252								
LTLQGLTIN	13910	IEELRQHLLRWGFTT	13253								
LVSAGIRKV	13911	RNMLTQLGCTLNFI	13254								
VDKLVSAIGI	13912	VDKLVSAIGIRKVLFL	13255								
YTGKVRQL	13913	NEQVDKLVSAIGIRKV	13256								
FRKQNPDIW	13914	SOIYPGIKVRQLCKL	13257								
FSFPQITLW	13915	TVSFSFPQITLWQRP	13259								
FTSTTVKAA	13916	GSNFTSTTVKACWW	13260								
IISDIQTK	13917	IIDIASDIQTKELQ	13261								
LAGRWPVKT	13918	LLKLGRWPVKTIHT	13262								
VQKIATESI	13919	TEAVQKIATESIIV	13263								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LRGAKALTD	13870	CKLLRGAKALTDIVP	13214					
LVSSGIRKV	13871	VDKLVSSGIRKKVFL	13215					
FLKLAGRW	13872	IAYFLKLAGRWPK	13216					
LALQDSGE	13873	AHLALQDSGSEVNI	13217					
LQDSGEVN	13874	HLALQDSGSEVNI	13218					
VKVHIDNG	13875	RWPVKVHIDNGSNF	13219					
WPKVHID	13876	AGRWPKVHIDNGS	13220					
YFLKLGR	13877	EIAYFLKLGRWPV	13221	0.0041				
ICGKAIGT	13878	LIEICGKAIGTIVL	13222					
IVAKEIVAS	13879	LPPIVAKEIVASCDK	13223					
LRWGFTTPD	13880	QHLLRWGFTTPDKKH	13224					
LEFGKILVA	13881	CTHLEFGKILVAHV	13225					
LKWGFTTPD	13882	EHLKKGFTTPDKKH	13226					
VILVAHVA	13883	EKGKILVAHVASGY	13227			0.2500	0.3000	
LAWVPAHKG	13884	KVYLAWVPAHKGIG	13228			1.6000	0.5200	
YDQILIEIC	13885	VRQYDQILIEICOKK	13229	0.0014	0.1400			
YLAWVPAHK	13886	EKVYLAWVPAHKGIG	13230	0.0010	1.4000			
IGQIRTKIE	13887	DLEIGQIRTKIEELR	13231		0.0012			
IGRNLLTQI	13888	VNIHGRNLLTQIGCT	13232					
LWQRPVTV	13889	QITLWQRPVTVIKIG	13233					
VSLTETNQ	13890	QKVVSLTETINQKTE	13234					
VYLAWVPAH	13891	KFKVYLAWVPAHKGIG	13235					
ICGHIKAGT	13892	LIEICGHIKAGTIVL	13236					
LRGTKALTE	13893	CKLLRGTKALTEVIP	13237					
LVNQIEQL	13894	ESELVNIQIEQLIKK	13238					
LVSQIEQL	13895	ESELVSIQIEQLIKK	13239					
YFSVPLDKD	13896	GDAYFSVPLDKDFRK	13240		0.0040			
IGRNMLTQI	13897	VNIHGRNMLTQIGCT	13241					
IKVRQLCKL	13898	YPIKIKVRQLCKLLRG	13242					
LWKGPAKLL	13899	RDPLWKGPAKLLWKG	13243					
LWQRPVTV	13900	QITLWQRPVTVIKIG	13244					
YAGIKVKQL	13901	SIYAGIKVKQLCKL	13245					
IWGTTPKFK	13902	SIVIWGTTPKFKLPI	13246					
LRHLKKGW	13903	IEELREHLKKGWFTT	13247					
VQPIQLPEK	13904	KWTVQPIQLPEKDSW	13248					
WQRPVTVIK	13905	ITLWQRPVTVIKIG	13249					
IIQAQPDRS	13906	ALGHQAQPDSESE	13250					
LOAHILALO	13907	KTELQAHILALQDSG	13251					
LVEICTEME	13908	IKALVEICTEMEKEG	13252					
LRQHLLRWG	13909	IEELRQHLLRWGFTT	13253					
LTQLGCTLN	13910	RNMLTQLGCTLNHPI	13254					
VKLVSAGI	13911	VDKLVSAIGIRKVLFL	13255					
YPIKVRQL	13912	NEQVDKLVSAIGIRKV	13256					
FRKQNPDI	13913	SIYPIKVRQLCKL	13257					
FSPQITLW	13914	LEPRKQNPDIYIQ	13258					
FTSTTVKAA	13915	IVSFSTTVKAAACWW	13259					
IIASDIQTK	13916	GSNFISIIASDIQTKELQ	13260					
LAGRWPKTK	13917	IIHIIASDIQTKELQ	13261					
VQKIATESI	13918	LLKLAGRWPKTKIHT	13262					
	13919	IEAVQKIATESIIVW	13263					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wB1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
F1P1STNNE	13920	YTAFT1P1STNNE1TPG	13264								
LEDINLPK	13921	DTVLEDINLPKWKIP	13265								
LTDIVPLTE	13922	AKALTDIVPLTEAE	13266								
LVTIKIGGO	13923	QRPLVTIKIGGQKLE	13267								
MRGAHTNDV	13924	YARMGAHTNDVKOL	13268								
VKTHITDNG	13925	RWPVKTHITDNGSNF	13269								
VQPVLPK	13926	KWTVQPVLPKDSW	13270								
WPVKTHITD	13927	AGRWPVKTHITDNGS	13271								
WQPLVTVK	13928	ITLWQPLVTVKIGG	13272								
WTVQPVLP	13929	PKWTVQPVLPKED	13273								
YTAFT1P1ST	13930	FRKYTAFT1P1STNNE	13274								
IDIASDIQ	13931	ERIDIASDIQ1KE	13275								
IDIASDI	13932	GERIDIASDIQTK	13276								
IVDIATDI	13933	GERIVDIATDIQTK	13277								
LEEINLPK	13934	DTVLEEINLPKWKIP	13278								
LOAYLALQ	13935	KTELQAYLALQDSG	13279								
LQKQIKIQ	13936	TKELQKQIKIQNFR	13280								
VDIATDIQ	13937	ERVDIATDIQ1KE	13281								
YDQIPEIC	13938	VROYDQIPEICGKK	13282								
FNPQITLW	13939	VPTFNPQITLWQRP	13283								
IGRNMLTQL	13940	VNIIGRNMLTQLGCT	13284								
ISRIGPENP	13941	EGKISRIGPENPYNT	13285								
LTEVIPLE	13942	TKALTEVIPLEEEAE	13286								
MESIVWKG	13943	KIAMESIVWKGTPK	13287								
VPRRKVKII	13944	IKVVPRRKVKHRDY	13288								
VSFSPQIT	13945	QGTVSFSFPQITLWQ	13289								
WYQLETEPI	13946	VKLWYQLETEPIVGA	13290								
YPGIKVKQL	13947	SOIYPGIKVKQLCKL	13291								
FQGEAREF	13948	NLAHQGEAREFPPE	13292								
LIEALLDTG	13949	GGQIEALLDTGADD	13293								
VSLTDITNQ	13950	QKVVSLTDITNQKTE	13294								
WETWWTDYW	13951	KETWETWWTDYWQAT	13295								
YAKMRTAHT	13952	TGKYAKMRTAHTNDV	13296								
YKNLKTGY	13953	QEPYKNLKTGYARM	13297								
LQLPPLERL	13954	PVPLQLPPLERLTD	13298								
VPLQLPPL	13955	AEPVPLQLPPLERLT	13299								
LYQSNPPPS	13956	IKFLYQSNPPPSPEG	13300								
VRIKILYO	13957	LKAVRIKILYQSNP	13301								
YQSNPPSP	13958	KFLYQSNPPSPSEGT	13302								
LQLPPIERL	13959	PVPLQLPPIERLTD	13303								
VPLQLPPIE	13960	AEPVPLQLPPIERLR	13304								
WNHPSQPK	13961	LEPNHPSQPKTAC	13305								
FLNKGGLIS	13962	QVCFLNKGGLISYGR	13306								
WKHPSQPK	13963	LEPWKHPSQPKTAC	13307								
YCKKCCFHC	13964	NNCYCKKCCFHCQVC	13308								
YCKKCCYHC	13965	TNCYCKKCCYHCQVC	13309								
WNHPSQPT	13966	LEPNHPSQPTTAC	13310								
MIVWQVDRM	13967	WQVMIVWQVDRMRIR	13311								
WQVMIVWQV	13968	ENRWQVMIVWQVDRM	13312								
WQVDRMRIR	13969	MIVWQVDRMRIRTWK	13313								

-0.0045

0.0032

1.9000

0.0690

-0.0043

0.0036

0.0059

3.3000

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTIPSTNNE	13920	YTAFTIPSTNNEIPG	13264					
LEEDINLPGK	13921	DIVLEEDINLPGKWKP	13265					
LTDIVPLTE	13922	AKALTDIVPLTEAE	13266					
LVTIKGGQ	13923	QRPLVTIKGGQKE	13267					
MRGAHTNDV	13924	YARMRGAHTNDVKQL	13268					
VKTIHTDNG	13925	RWPVKTIHTDNGSNF	13269					
VQPIVLPK	13926	KWTVQPIVLPKDSW	13270					
WPVKTIHTD	13927	AGRWVPVKTIHTDNGS	13271					
WQRPVTVVK	13928	FLWQRPVTVVKIGG	13272					
WTVQPIVLP	13929	PDKWTVQPIVLPKED	13273					
YTAFTIPST	13930	FRKYTAFTIPSTNNE	13274					
IDIIASDIQ	13931	ERIDIIASDIQIKE	13275					
IIDIIASDI	13932	GERIDIIASDIQIK	13276					
IVDIIATDI	13933	GERIVDIIATDIQIK	13277		0.0026			
LEENLPGK	13934	DIVLEENLPGKWKP	13278					
LQAIYLALQ	13935	KTELQAIYLALQDSG	13279					
LQKQIKIQ	13936	IKELQKQIKIQNPK	13280					
VDIIATDIQ	13937	ERIVDIIATDIQIKE	13281					
YDQPIEC	13938	VRQYDQPIECGKK	13282					
FNFPQITLW	13939	VPTFNFPQITLWQRP	13283					
IGRNMLTQL	13940	VNIIGRNMLTQLGCT	13284					
ISRIGPENP	13941	EKGISRIGPENPYNT	13285					
LTEVIPLTE	13942	IKALITEVIPLTEAE	13286					
MESIVWIK	13943	KIAMESIVWIKTIPK	13287					
VPRKVKII	13944	IKVVPKRKVKIIRDY	13288					
VSFSPQIT	13945	QGITVSFSFPQITLWQ	13289					
WYQLETEPI	13946	VKLWYQLETEPIVGA	13290					
YQGIKVKQL	13947	SQIYQGIKVKQLCKL	13291					
FPQGEAREF	13948	NLAFFQGEAREFPE	13292					
LIEALLDTG	13949	GGQIEALLDTGADD	13293					
VSLDTITNQ	13950	QKVVSLDTITNQKTE	13294					
WETWWTDYW	13951	KETWETWWTDYWQAT	13295					
YAKMRTAHT	13952	TGKYAKMRTAHTNDV	13296					
YKNLKTGKY	13953	QEPYKNLKTGKYARM	13297					
LQLPLERL	13954	PVPLQLPLPLERLTD	13298					
VPLQLPPL	13955	AEPVPLQLPPLERLT	13299					
LYQSNPPPS	13956	IKFLYQSNPPPSPEG	13300					
VRIKILYQ	13957	LKAVRIKILYQSNP	13301					
YQSNPPSP	13958	KFLYQSNPPSPPEGT	13302					
LQLPPLERL	13959	PVPLQLPPLERLTD	13303					
VPLQLPPIE	13960	AEPVPLQLPPIERLR	13304					
WNIIPGSQPK	13961	LEPWNIIPGSQPKTAC	13305					
FLNKGLGIS	13962	QVCFLNKGLGISYGR	13306					
WKIIPGSQPK	13963	LEPWKIPGSQPKTAC	13307					
YCKKCCFHC	13964	NNCYCKKCCFHCQVC	13308					
YCKKCCYHC	13965	INCYCKKCCYHCQVC	13309					
WNIIPGSQPT	13966	LEPWNIIPGSQPTTAC	13310					
MIVWQVDRM	13967	WQVMIVWQVDRMRIR	13311					
WQVMIVWQV	13968	ENRWQVMIVWQVDRM	13312	0.0018	0.1200	0.1500	0.2900	
WQVDRMRIR	13969	MIVWQVDRMRIRTWK	13313					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LOYLALTAL	13970	VGSLOYLALTALIKP	13314								
LGHGVSIEW	13971	DWHLGHGVSIEWRLR	13315								
VDRMRITW	13972	VWQVDRMRITWNSL	13316								
YFDCFESA	13973	HLYYFDCFESAIRN	13317								
YWGHTGER	13974	ITTYWGLHTGERDWH	13318								
IRWNSLVK	13975	RMRTWNSLVKHHM	13319								
LGQGVSEW	13976	DWILGQGVSEWRKK	13320								
LVKHHMYVS	13977	WNSLVKHHMYVSKKA	13321								
IPLGEARLV	13978	EVHPLGGEARLVVRT	13322								
LVKHHMYIS	13979	WKS LVKHHMYISGKA	13323								
YLALTALIK	13980	SLOYLALTALIKPKK	13324								
IRTKSLVK	13981	RMRTWKS LVKHHM	13325								
LADQLHLY	13982	DPDLADQLHLYYFD	13326								
LALTALIKP	13983	LOYLALTALIKPKKI	13327								
VDPGLADQL	13984	STQVDPGLADQLIHL	13328								
LYYFDCFSE	13985	LHILYYFDCFSESAL	13329								
FSESARKA	13986	FDCFSESARKAILG	13330								
LADQLHHMI	13987	EPGLADQLHHMIYFD	13331								
WQVDRMKIR	13988	LIVWQVDRMKIRTWN	13332								
FSDSAIRKA	13989	FDCFSDSAIRKAILG	13333								
FSESARNA	13990	FDCFSESARNAILG	13334								
IVSPRCEYQ	13991	LGHVSPRCEYQAGH	13335								
LOYLALAAL	13992	VGSLOYLALAALITP	13336								
VDRMKIRTW	13993	VWQVDRMKIRTWNSL	13337								
YWGLQTGER	13994	IKTYWGLQTGERDWH	13338								
IPGLDARLV	13995	EVHPLGDARLVIT	13339								
LOYLALKAL	13996	VGSLOYLALKALVTP	13340								
WQVDRMRIN	13997	MIVWQVDRMRINTWK	13341								
IKPKKIKPP	13998	TALIKPKKIKPLPS	13342								
VDRMRINTW	13999	VWQVDRMRINTWKS	13343								
IGCQHSRIG	14000	HFRIGCQHSRIGTR	13344								
WTELELEL	14001	YNEWTELELELKE	13345								
ILQQLFIH	14002	IIRLQQLFIHFRI	13346								
FIHFRIGCQ	14003	QLLFIHFRIGCQHSR	13347								
YNEWTELEL	14004	REPYNWTELELEL	13348								
FPRPWLHGL	14005	VRHFRPWLHGLGQH	13349								
WEGVEAIR	14006	GDTWEGVEAIRILO	13350								
LEELKEAV	14007	LELEELKEAVRHF	13351								
WAGVEAIR	14008	GDTWAGVEAIRILO	13352								
YGDTWAGVE	14009	YETYGDTWAGVEAIL	13353								
IGCRHSRIG	14010	HFRIGCRHSRIGTR	13354								
FIHFRIGCQ	14011	QLLFIHFRIGCRHSR	13355								
YGDTWTGVE	14012	QLLFVHFRIGCQHSR	13356								
FPRIWLHSL	14013	YETYGDTWTGVEAIL	13357								
WALELEEL	14014	VRHFRPWLHSLGQH	13358								
LVTLSSSK	14015	YNEWALELEELKNE	13359								
VTLLSSSK	14016	EEWLVTLLSSSKLDO	13360								
IIAIVVWTI	14017	EWLVTLSSSKLDOG	13361								
VYRIVIVA	14018	VVAIAIVVWTIVFI	13362								
	14019	LAKVDYRIVIVAFIV	13363								

0.0200

0.0054

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LQYALATL	13970	VGSQYLALATLAKP	13314					
LGHGVSEW	13971	DWHLGHGVSEWRLR	13315					
VDRMRITW	13972	VWQVDRMRITWNSL	13316					
YFDFSES	13973	HLYYFDFSESAIN	13317					
YWGLHTGR	13974	ITTYWGLHTGERDWH	13318					
RTWNSLVK	13975	RMRIKRTWNSLVKHHM	13319					
LQGVSEW	13976	DWHLQGVSEWKKK	13320					
LVKHHMYIS	13977	WNSLVKHHMYVSKKA	13321					
PLGLEARLV	13978	EVHPLGLEARLVRT	13322					
LVKHHMYIS	13979	WKSLLVKHHMYISGKA	13323					
YLALATLIK	13980	SLQYLALATLIKPKK	13324					
IRTWKSLVK	13981	RMRIKRTWKSLLVKHHM	13325					
LADQLHLY	13982	DPLADQLHLYYFD	13326					
LALTALIKP	13983	LQYLALATLIKPKKI	13327					
VDPLADQL	13984	STQVDPGLADQLHL	13328					
LYYFDFSE	13985	HLHYFDFSESAT	13329					
FSESARKA	13986	FDCFSESARKKAILG	13330					
LADQLHHI	13987	EPGLADQLHHIHYFD	13331					
WQVDRMKIR	13988	LIVWQVDRMKIRTWN	13332					
FSDSAIRKA	13989	FDCFSDSAIRKAILG	13333					
FSESARNA	13990	FDCFSESARNAILG	13334					
IVSPREYQ	13991	LGHVSPREYQAGH	13335					
LQYALALAL	13992	VGSQYLALALALTP	13336					
VDRMKIRTW	13993	VWQVDRMKIRTWNSL	13337					
YWGLQTGR	13994	IKTYWGLQTGERDWH	13338					
PLGDARLV	13995	EVHPLGDARLVIT	13339					
LQYALALK	13996	VGSQYLALKALVTP	13340					
WQVDRMRIN	13997	MIVWQVDRMRINTWK	13341					
IKPKKIKPP	13998	LALIKPKKIKPLPS	13342					
VDRMRINTW	13999	VWQVDRMRINTWKSLL	13343					
IGQHSRIG	14000	HFRIQCQHSRIGTR	13344					
WTELEEL	14001	YNEWTELEELKSE	13345					
ILQQLFIH	14002	IIRLQQLFIHFRI	13346					
FHFRIQCQ	14003	QLLFHFRIQCQHSR	13347					
YNEWTELE	14004	REPYNWTELELEEL	13348					
FPRPWLHGL	14005	VRHPRPWLHGLGQH	13349					
WEGVEAIR	14006	GDTWEGVEAIRILQ	13350					
LEELKSEAV	14007	LELEELKSEAVRHF	13351					
WAGVEAIR	14008	GDTWAGVEAIRILQ	13352					
YGDTWAGVE	14009	YETYGDTWAGVEAI	13353					
IGCRHSRIG	14010	HFRIQCQHSRIGTR	13354					
FHFRIQCR	14011	QLLFHFRIQCQHSR	13355					
FVIFRIGCQ	14012	QLLFVIFRIGCQHSR	13356					
YGDTWTGVE	14013	YETYGDTWTGVEAI	13357					
FPRIWLHSL	14014	VRHPRWLHSLGQH	13358					
WALELEEL	14015	YNEWALELEELKNE	13359					
LVTLLSSSK	14016	EEWLVTLLSSSKLDQ	13360					
VTLLSSSKL	14017	EWLVTLLSSSKLDQ	13361					
IIIVVWTI	14018	VVAIIIVVWTIVI	13362					
VDYRIVIVA	14019	LAKVDYRIVIVAHV	13363					

0.0084

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w01	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LRQRKIDRL	14020	RKILRQRKIDRLIDR	13364								
IVVWTTIVFI	14021	IIAIVVWTTIVFIEYR	13365								
VVWTTIVFIE	14022	IAIVVWTTIVFIEYRK	13366								
IEYRKILRQ	14023	IVFIEYRKILRQRKI	13367								
IIAIVALVV	14024	SLYLAIIVALVVAII	13368								
WTTIVFIEYR	14025	IVVWTTIVFIEYRKIL	13369								
LAIVALVVA	14026	LQILAIVALVVAGII	13370								

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LRORKIDRL	14020	KKILRQRKIDRLIDR	13364					
IVVWTVTFI	14021	IIAIVVWTVTFIEYR	13365					
VVWTVTFIE	14022	IAIVVWTVTFIEYRK	13366					
IEYRKILRQ	14023	IVHIEYRKILRQRKI	13367					
IIAIVALVV	14024	SLYLIIAIVALVVAII	13368					
WTVTFIEYR	14025	IVVWTVTFIEYRKIL	13369					
LAIVLVVA	14026	LQILAIVALVVAGII	13370					

Table XXa
HIV DR 3a Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	VPTDPNQE	14027	53	83	HACVPTDPNQEVL	13371	85	12	19
ENV	YLKDDQLLG	14028	31	48	VERYLKDQQLGIWG	13372	669	18	28
ENV	MIHEDISLW	14029	29	45	VEOMHEDISLWDS	13373	114	17	28
ENV	VSEFPIPH	14030	29	45	CPKVSFPIPHYCA	13374	250	18	28
ENV	LAVERYLKD	14031	26	41	ARVLAVERYLKDQQL	13375	664	15	23
ENV	VKIEPLGVA	14032	23	36	YKVVKIEPLGVAPTK	13376	52	22	34
ENV	VWKEATTL	14033	22	34	GVPVWKEATTLFCA	13377	849	19	30
ENV	LAWDDLSL	14034	20	31	FLALAWDDLSLCLF	13378	737	07	11
ENV	LIEESQNOQ	14035	20	31	LYTLIEESQNOQEN	13379	892	07	23
ENV	LGWEGGLYL	14036	09	29	GLRLGWEGGLYLWNL	13380	753	11	11
ENV	LELDKWSL	14037	18	28	QELLELDKWSLWNW	13381	669	11	17
ENV	YLKDQQLG	14038	18	28	VERYLRDQQLGIWG	13382	492	12	19
ENV	MWQEVGKAM	14039	15	23	IINMWQEVGKAMYAP	13383	827	08	13
ENV	IEEGGERD	14040	13	20	PEGIEEGGERDRDR	13384	212	01	2
ENV	MINNENGTN	14041	01	19	INEMNNENGTNSTW	13385	827	02	3
ENV	IEEGGEQD	14042	12	19	LGRIIEEGGEQDKNR	13386	309	04	6
ENV	LAEEVYIR	14043	12	17	NGSLAEEVYIRSEN	13387	753	05	8
ENV	LALDKWASL	14044	11	17	QDLLALDKWASLWNW	13388	664	10	16
ENV	LAVERYLRD	14045	11	16	ARVLAVERYLRDQQL	13389	317	03	5
ENV	IRSENLTNN	14046	10	16	ELIIRSENLTNNVKT	13390	721	03	5
ENV	MEWEREIDN	14047	10	16	MTWMEWEREIDNYS	13391	223	18	28
GAG	INEEAEWD	14048	55	86	KETINEEAEWDRHLH	13392	383	36	56
GAG	FSPEVPMF	14049	54	84	EKAFSPEVPMFSAL	13393	218	09	14
GAG	VLAEMSQV	14050	33	52	KARVLAEMSQVTSNS	13394	176	28	44
GAG	MLKDTINEE	14051	32	50	AMQMLKDTINEEAAE	13395	325	22	34
GAG	VVEEKAFSP	14052	28	44	WVKVVEEKAFSPEVI	13396	176	20	31
GAG	LRAEQATQE	14053	27	42	FKTLRAEQATQEVKN	13397	383	03	5
GAG	MLKETINEE	14054	23	36	AMQMLKETINEEAAE	13398	103	09	14
GAG	VIEKAFSP	14055	21	33	WVKVIEKAFSPEVI	13399	325	10	16
GAG	VLAEMSQA	14056	16	25	KARVLAEMSQA	13400	369	59	92
GAG	IEEEQNKSK	14057	15	23	LDKIEEEQNKSKKA	13401	236	28	44
GAG	LRAEQATQD	14058	14	22	FKTLRAEQATQDVKN	13402	420	29	45
GAG	LRAEQASQE	14059	12	19	YKTLRAEQASQEVKN	13403	684	58	91
NEF	YFPDWQNYT	14060	36	56	TQGYFPDWQNYTPGP	13404	838	55	86
NEF	FLKEKGGLE	14061	30	47	LSHFLKEKGGLEGLI	13405	210	26	41
NEF	FFPDWQNYT	14062	26	41	LSFFLKEKGGLEGLI	13406	781	32	50
NEF	VSRDLKHG	14063	17	27	TOGFFPDWQNYTPGP	13407	794	47	73
POL	YMDDLTVGS	14064	11	17	VGAVSRDLKKGHAI	13408	375	28	44
POL	IGPENPNT	14065	62	97	IYQYMDLLYVGS	13409	1017	36	56
POL	LHPDKWTVQ	14066	60	94	ISKIGPENPNTPVF	13410			
POL	IPAEVQET	14067	60	94	GVELHPDKWTVQPIQ	13411			
POL	IVTDSQYAL	14068	59	92	EVNIVTDSQYALGII	13412			
POL	LTEKIKAL	14069	58	91	AEVIPAETGQETAYF	13413			
POL	IEAEVPAE	14070	56	88	QWPLTEKIKALTEI	13414			
POL	LFLDGIDKA	14071	55	86	SGYIEAEVPAETGQ	13415			
POL	VAKIVASC	14072	55	86	RKVLFLDGIDKAQEE	13416			
POL	LKGEAMHGQ	14073	54	86	PPVVAKEIVASCDC	13417			
POL	VGSDLIEGQ	14074	53	83	KCOLKGEAMHIGQVDC	13418			
POL	IIRDYQKQM	14075	53	83	DLYVGSDLIEGQHRA	13419			
POL		14076	50	78	KAKIIRDYQKQMAGD	13420			

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	MASDFNLPP	14077	47	73	WRAMASDFNLPPVVA	13421	771	24	38
POL	FYVDGAANR	14078	43	67	AETFYVDGAANRETK	13422	629	33	52
POL	IHTDNGSNF	14079	42	66	VKVIHTDNGSNFTSA	13423	862	17	27
POL	ILKEPVHGV	14080	41	64	NREILKEPVHGVYD	13424	495	36	56
POL	IYQEPKNL	14081	40	63	TYQIYQEPKNLKTG	13425	530	39	61
POL	VYDPSKDL	14082	39	61	VHGYYVDPSKDLAE	13426	506	26	41
POL	YVTDGRQK	14083	39	61	KAGYVTDGRQKVVS	13427	646	19	30
POL	LTEAELEL	14084	37	58	IVPLTEAELELAEN	13428	481	12	19
POL	VIQDNDIK	14085	37	58	GAVVIQDNDIKVVP	13429	999	37	58
POL	IATDIQKE	14086	35	55	IDIIATDIQKELOK	13430	953	22	34
POL	INNETPGIR	14087	32	51	IPSINNETPGIRYOY	13431	321	31	48
POL	LIAEQKOG	14088	30	47	SKDLIAEQKOGQGG	13432	514	09	14
POL	ICTEMEKEG	14089	28	44	LVEICTEMEKEGKIS	13433	221	14	22
POL	VGAETFYVD	14090	28	44	EPVGAETFYVDGAA	13434	624	20	31
POL	IQKETWETW	14091	27	42	RLPIQKETWETWTTD	13435	582	09	14
POL	IKQIEGIPY	14092	26	41	WAGIKQIEGIPYNPO	13436	884	21	33
POL	MAGDDCVAG	14093	25	39	GKQMGDDCVAGRQD	13437	1025	23	36
POL	IKKEKVYLA	14094	20	31	EQLIKKEKVYLAWVP	13438	715	19	30
POL	VPLDKDFRK	14095	19	30	GKQMGDDCVASROD	13439	1025	19	30
POL	IQKEFGIPY	14096	18	28	YFSVPLDKDFRKTYA	13440	304	18	29
POL	LEKEPVGA	14097	16	25	WAGIQKEPVGAETF	13441	884	11	17
POL	YQLEKEPIV	14098	16	25	WYQLEKEPIVGAETF	13442	618	16	25
POL	IQKETWEAW	14099	15	23	KLWYQLEKEPIVGAE	13443	582	05	25
POL	FSSEQTRAN	14100	14	22	AREFSSEQTRANSPPT	13444	582	10	16
POL	IASDIQKE	14101	14	22	IDIIASDIQKELOK	13445	14	09	14
POL	ILIEICGKK	14102	14	22	VQKIATESIVWGKT	13446	953	11	17
POL	VLEINLPG	14103	14	22	YDQILIEICGKKAIG	13447	564	11	20
POL	IKKEKVYLS	14104	14	22	DDTVLEINLPGKWK	13448	146	13	17
POL	VLEDINLPG	14105	13	20	EQLIKKEKVYLSWVP	13449	116	11	11
POL	VLEKDSWT	14106	13	20	DDTVLEINLPGKWK	13450	715	07	20
POL	VIQDSEIK	14107	12	19	QPIVLPEKDSWTVND	13451	116	13	20
POL	IKDYGKQM	14108	11	17	GAVVIQDSEIKVVP	13452	431	13	20
POL	VERETETDP	14109	11	17	KAKIKDYGKOMAGA	13453	999	12	19
TAT	LTEDRWKNP	14110	11	17	KEKVERETETDPAVQ	13454	1017	06	9
VIF	YYFDCSES	14111	11	44	VKKLTEDRWKNPQKT	13455	95	01	2
VIF	LVEDRWKNP	14112	28	31	IHLVYFDCSESAR	13456	175	09	14
VIF	IDPDLADQL	14113	20	17	VOKLVEDRWKNPQKT	13457	112	14	22
VIF	LKNEAVRHIF	14114	10	16	STQIDPDLADQLIHL	13458	175	04	6
VPR	YIYETGDT	14115	18	28	LEELKNEAVRHIFPRP	13459	100	10	16
VPR	LKQEAARHIF	14116	15	23	LEELKNEAVRHIFPRP	13460	23	10	16
VPR	YIYETGDT	14117	14	22	LQYIYETGDTWAG	13461	42	07	11
VPR	LKQEAARHIF	14118	11	17	LEELKQEAARHIFPRP	13462	42	07	11
VPR		14119	11	17		13463	23	06	9

Table XXb

HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w8I	DR2w2I2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VTDPNPQE	14027	IIACVPTDPNPQEVVL	13371								
YLDQQLLG	14028	VERYLKDQQLLGHWG	13372								
MIHDIISLW	14029	VEOMHIEDIISLWDQS	13373								
VSFEPIPIII	14030	CPKVSFEPIPIHYCA	13374								
LAVERYLKD	14031	ARVLAVERYLKDQQL	13375								
VKIEPLGVA	14032	YKVVVKIEPLGVAPTK	13376								
VWKEATTTL	14033	GPPVWKEATTTLFCF	13377								
LAWDDLRLS	14034	FLALAWDDLRLSLCF	13378								
LIIESNQOQ	14035	IYTLIESNQOQEKH	13379								
LGWIECLKYL	14036	GLRLGWIECLKYLWNL	13380								
LELDKWASL	14037	QELLELDKWASLWNW	13381								
YLRDQQLG	14038	VERYLRDQQLLGHWG	13382								
MWQEVGKAM	14039	IINMWQEVGKAMYAP	13383								
IEEKGGERD	14040	PEGIEEGGERDRDR	13384								
MNENNGTN	14041	INEMNENNGTNTW	13385								
IEEKGGEQD	14042	LGRIIEEGGEQDKNR	13386								
LAEEVIVIR	14043	NGSLAEEVIVIRSEN	13387								
LALDKWASL	14044	QDILLALDKWASLWNW	13388								
LAVERYLRD	14045	ARVLAVERYLRDQQL	13389								
IRSENLTNN	14046	EHIRSENLTNNVKT	13390								
MEWERHIDN	14047	MTWMEWERHIDNYTS	13391								
INEEAAEWD	14048	KETINEEAAEWDRLH	13392								
FSPEVPMF	14049	EKAFSPEVPMFSAL	13393	0.0086	0.0015		-0.0130	0.0340		-0.0010	
VLAFAMSQV	14050	KARVLAFAMSQVTS	13394	0.0080				0.0120			
MLKDTINEE	14051	AMQMLKDTINEEAAE	13395	0.0006				0.0016			
VVEKAFSP	14052	WVKVVEKAFSPEVI	13396								
LRAEQATQE	14053	FKTLRAEQATQEVKN	13397								
MLKETINEE	14054	AMQMLKETINEEAAE	13398								
VIEKAFSP	14055	WVKVIEKAFSPEVI	13399								
VLAFAMSQA	14056	KARVLAFAMSQASGA	13400								
IEEEQNRSK	14057	LDKIEEENQSKKKA	13401								
LRAEQATQD	14058	FKTLRAEQATQDVKN	13402								
YFPDWQNYT	14059	YKTLRAEQASQEVKN	13403				-0.0017				
FLKEGGGLE	14061	TQGYFPDWQNYTPGP	13404								
FPPDWQNYT	14062	LSHFLKEKGGGLEGL	13405								
YMDPLYVGS	14063	LSFFLKEKGGGLDGL	13406								
VSRDLEKHG	14064	TQGFPPDWQNYTPGP	13407								
IGPENPYNT	14066	VGAVSRDLEKHGAT	13408								
LHPDKWTVQ	14067	IYQYMDPLYVGSDE	13409	0.0001	-0.0014		-0.0130	-0.0026		-0.0006	
IPAEITQET	14068	ISKIGPENPYNTPVF	13410								
LTEEKIKAL	14070	EVNIVTDSQYALGII	13412	0.0002	0.0034	-0.0010	0.4100	-0.0055		-0.0006	
IEAEVPAE	14071	AEVIPAEITQETAYF	13413				-0.0033				
LFLDGIDKA	14072	QWPLTEEEKIKALTEI	13414								
VAKIVASC	14073	SGYIEAEVIPAEITQ	13415								
VGSDELEIGQ	14074	RKVLFLDGDIDKAOEE	13416								
IRDYGKOM	14075	PPVVAKEIVASCDC	13417	0.0001	-0.0021		-0.0130	0.0085		-0.0006	
	14076	KCQLKGEAMHGQVDC	13418				-0.0017				
		DLYVGSDELEIGQHRA	13419								
		KAKIIRDYGKOMAGD	13420								

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VPTDNPQE	14027	IACVPTDNPQEVVL	13371					
YLDQQLLG	14028	VERYLKDQQLGIWG	13372					
MIRHDSLW	14029	VEQMIEDISLWDQS	13373					
VSFEPIPH	14030	CPKVSFEPIPIHYCA	13374					
LAVERYLKD	14031	ARVLAVERYLKDQQL	13375					
VKIEPLGVA	14032	YKVVKIEPLGVAPTK	13376					
VWKEATITL	14033	GVVWKEATITTLFCA	13377					
LAWDDLRLS	14034	FLALAWDDLRLSLCLF	13378					
LIEISQNOQ	14035	IYTLIEISQNOQIEKN	13379					
LGWGLKYL	14036	GLRLGWGLKYLWNL	13380					
LELDKWASL	14037	QELLELDKWASLWNL	13381					
YLRDQQLG	14038	VERYLRDQQLGIWG	13382					
MWQEVGKAM	14039	INMWQEVGKAMYAP	13383					
IEEGGERD	14040	PEGIEEGGERDRDR	13384					
MNENNGTN	14041	INENNNENNGTNSTW	13385					
IEEGGEQD	14042	LGRIIEEGGEQDKNR	13386					
LAEEVVIR	14043	NGSLAEEVVIRSEN	13387					
LALDKWASL	14044	QDLLALDKWASLWNL	13388					
LAVERYLRD	14045	ARVLAVERYLRDQQL	13389					
IRSENLTN	14046	EHIRSENLTNVKT	13390					
MEWEREIDN	14047	MTWMEWEREIDNYTS	13391					
INEFAEWD	14048	KETINEEAAEWDRH	13392		0.0023			
FSPEVPMF	14049	EKAESPEVPMFSAL	13393		0.0025			
VLAAMSQV	14050	KARVLAAMSQVTSN	13394					
MLKDTINEE	14051	AMQMLKDTINEAAE	13395					
VVEEKAFSP	14052	WVKVVEEKAFSPEVI	13396		0.0003			
LRAEQATQE	14053	FKTLRAEQATQEVKN	13397					
MLKETINEE	14054	AMQMLKETINEAAE	13398					
VIEEKAFSP	14055	WVKVIEEKAFSPEVI	13399					
VLAAMSQA	14056	KARVLAAMSQASGA	13400					
IEEQNKSK	14057	LDKIEEQNKSKKA	13401					
LRAEQATQD	14058	FKTLRAEQATQDVKN	13402					
LRAEQASQE	14059	YKTLRAEQASQEVKN	13403					
YFPDWQNYT	14060	TQGYFPDWQNYTPGP	13404					
FLKEKGLE	14061	LSHFLKEKGLEGLI	13405					
FLKEKGGLD	14062	LSFFLKEKGGLDGLI	13406					
FFPDWQNYT	14063	TQGFPPDWQNYTPGP	13407					
VSRLDKIIG	14064	VGAVSRDLKLEKHGAT	13408					
YMDLLYVGS	14065	IYQYMDLLYVGSLE	13409					
IGPENPYNT	14066	ISKIGPENPYNTPVF	13410		-0.0005			
LHPDKWTVQ	14067	GYELHPDKWTVQPIQ	13411					
IVTDSQYAL	14068	EYNIIVTDSQYALGII	13412	0.0108	-0.0014	-0.0009		
IPATGQET	14069	AEVIPATGQETAYF	13413					
LTEEKIKAL	14070	QWPLTEEKIKALTEI	13414					
IEAEVIPAE	14071	SGYIEAEVIPAETGQ	13415					
LFLDGIDKA	14072	RKVLFDGIDKAQEE	13416					
VAKFIVASC	14073	PPVVAKEIVASCDC	13417					
LKGEAMHGO	14074	KCOLKGEAMHGOVDC	13418		0.0015			
VGSDLEIGQ	14075	DLYVGSDLEIGQHRA	13419					
IIRDYGKQM	14076	KAKIIRDYGKQMAGD	13420					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w2l2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
MASDFNLPP	14077	WRAMASDFNLPPVVA	13421								
FYVDGAANR	14078	AETFYVDGAANRETK	13422	0.0021	-0.0005	0.0046	0.3900	0.0150		-0.0006	
IHTDNGSNF	14079	VKVHTDNGSNFTSA	13423								
ILKEPVIHV	14080	NRELKEPVIHVYVD	13424								
IYQEPKNL	14081	TYQIYQEPKNLKTG	13425	0.3000	0.1500	-0.0014	0.1000	0.1900	0.0300	-0.0007	0.0230
VYDPSKDL	14082	VHGYYDPSKDLIAE	13426				-0.0017				
YVTDGRQK	14083	KAGYVTDGRQKVV	13427								
LTEEALEL	14084	IVPLTEEALELAEN	13428								
VIQDNDIK	14085	GAVVIQDNDIKVVP	13429	0.0033	0.0280	0.0014	0.3000	-0.0055		-0.0006	
IATDIQTK	14086	IDHATDIQTKELQ	13430								
INNETPGIR	14087	IPSINNETPGIRYQY	13431								
LIAEQKOG	14088	SKDLIAEQKOGQ	13432								
ICTEMEKEG	14089	LVEICTEMEKEGKIS	13433				-0.0017				
VGAETFYVD	14090	EPIVGAETFYVDGAA	13434								
IQKETWETW	14091	RLPIQKETWETWWT	13435								
IKQEFGIPY	14092	WAGIKQEFGIPYNPQ	13436	0.0018	0.0018	0.1600	1.0000	0.0140		-0.0006	
MAGDDCVAG	14093	GKQMGDDCVAGRQD	13437	0.6400	0.0800	0.0059	0.0300	4.1000		0.0058	-0.0045
IKKEKVLA	14094	EQLIKKEKVLAWVP	13438								
MAGDDCVAS	14095	GKQMGDDCVASRQD	13439								
VPLDKDFRK	14096	YESVPLDKDFRKYTA	13440								
IQKEFGIPY	14097	WAGIQKEFGIPYNPQ	13441								
LEKEPIVGA	14098	WYQLEKEPIVGAET	13442								
YQLEKEPIV	14099	KLWYQLEKEPIVGA	13443								
IQKETWEAW	14100	KLPIQKETWEAWWTE	13444								
FSSEQTRAN	14101	AREFSSEQTRANSP	13445								
IASDIQTK	14102	IDHIASDIQTKELQ	13446								
IATESIVIV	14103	VQKIATESIVIVGKT	13447								
ILIEICGKK	14104	YDQILIEICGKKAIG	13448								
VLEINLPG	14105	DDTVLEINLPGKW	13449								
IKKEKVLS	14106	EQLIKKEKVLSWVP	13450								
VLEDINLPG	14107	DDTVLEDINLPGWK	13451								
VLEPKDSWT	14108	QPIVLEPKDSWTVD	13452								
VIQDNSEIK	14109	GAVVIQDNSEIKVVP	13453								
IKDYGKOM	14110	KAKIKDYGKOMAGA	13454								
VERETETDP	14111	KEKVERETETDPAVQ	13455								
LTEDRWNKP	14112	VKKLTEDRWNKPQKT	13456								
YYFDCFSES	14113	IHLYYFDCFSESAR	13457								
LVEDRWNKP	14114	VQKLVEDRWNKPQKT	13458								
IDPDLADQL	14115	STQIDPDLADQLIHL	13459								
LKNEAVRHF	14116	LEELKNEAVRHFPRP	13460								
LKSEAVRHF	14117	LEELKSEAVRHFPR	13461								
YIYETGDT	14118	LGOYIYETGDTWAG	13462								
LKQEAVRHF	14119	LEELKQEAVRHFPR	13463								

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
MASDFNLPP	14077	WRAMASDFNLPPVVA	13421					
FYVDGAANR	14078	AETFYVDGAANRETK	13422	-0.0002	-0.0014	0.0035		
HIIDNCSNF	14079	VKVHIIDNCSNFTSA	13423					
ILKEPVIIGV	14080	NREILKEPVIIGVYVD	13424	0.0120	0.0033	0.0010	0.0210	
IYQEPKNL	14081	TYQIYQEPKNLKTG	13425					
VYVDPSKDL	14082	VHGVYVDPSKDLIAE	13426					
YVTDGRQK	14083	KAGYVTDGRQKVVS	13427					
LTEAELEL	14084	IVPLTEAELELAEN	13428					
VIQDNSDIK	14085	GAVVIQDNSDIKVVP	13429	0.0447	-0.0014	-0.0009		
IATDIQTKE	14086	IDIIATDIQTKELOK	13430					
INNETHGIR	14087	IPSINNETHGIRYQY	13431					
LIAEIOKOG	14088	SKDLIAEIOKOGQGO	13432					
ICTEMEKEG	14089	LVEICTEMEKEGKIS	13433					
VGAETFYVD	14090	EPIVGAETFYVDGAA	13434					
IQKETWETW	14091	RLPIKETWETWWTID	13435					
IKQEFGIPY	14092	WAGIKQEFGIPYNPQ	13436	0.0123	-0.0014	-0.0009		
MAGDDCVAG	14093	GKQMGDDDCVAGROD	13437					
IKKEKVYLA	14094	EQLIKKEKVYLAWVP	13438	-0.0003	-0.0005	-0.0015	0.0011	
MAGDDCVAS	14095	GKQMGDDDCVASROD	13439					
VPLDKDFRK	14096	YFSVPLDKDFRKYTA	13440					
IQQEFGIPY	14097	WAGIQQEFGIPYNPQ	13441					
LEKEPIVGA	14098	WYQLEKEPIVGAETF	13442					
YQLEKEPIV	14099	KLWYQLEKEPIVGAE	13443					
IQKETWEAW	14100	KLPQKETWEAWWTE	13444					
FSSEQTRAN	14101	AREFSSEQTRANSPT	13445					
IASDIQTKE	14102	IDIIASDIQTKELOK	13446					
IATESIWIW	14103	VQKIATESIWIWGKT	13447					
ILIEICGKK	14104	YDQILIEICGKKAIG	13448					
VLFEINLPG	14105	DDTVLFEINLPGKWK	13449					
IKKEKVYLS	14106	EQLIKKEKVYLSWVP	13450					
VLEDINLPG	14107	DDTVLEDINLPGKWK	13451					
VLPEKDSWT	14108	QPIVLPEKDSWTVND	13452					
VIQDNSEIK	14109	GAVVIQDNSEIKVVP	13453					
IKDYGKOM	14110	KAKIKDYGKOMAGA	13454					
VERETETDP	14111	KEKVERETETDPAYQ	13455					
LTEDRWNKP	14112	VKKLTEDRWNKPKPT	13456					
YVFDCFSES	14113	IHLIYVFDCFSESAR	13457					
LVEDRWNKP	14114	VQKLVEDRWNKPKPT	13458					
IDPLADQL	14115	STQIDPLADQLIHL	13459					
LKNEAVRHF	14116	LEELKNEAVRHFPRP	13460					
LKSEAVRHF	14117	LEELKSEAVRHFPRP	13461					
VIYETGDT	14118	LQQVIYETGDTWAG	13462					
LKQEA VRHF	14119	LEELKQEA VRHFPRP	13463					

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	MRDNRSEL	14120	40	63	GGDMRDNRSELKY	13464	550	37	58
ENV	LTVQARQLL	14121	36	56	SITLTVQARQLLSGI	13465	620	27	42
ENV	IEAQOHLQ	14122	35	55	LRAIEAQOHLQLTV	13466	642	34	53
ENV	IIGDIROAH	14123	27	44	TGEIGDIRQAHICNI	13467	370	07	11
ENV	VEREKRAVG	14124	23	37	RRVVEREKRAVGIGA	13468	582	11	17
ENV	MVEQMIEDI	14125	23	36	KNNMVEQMIEDIISL	13469	110	19	30
ENV	AWDDLRLSC	14126	20	31	LALAWDDLRLSLCLS	13470	850	18	28
ENV	LEITTHISFN	14127	20	31	GGDLEITTHISFNCRG	13471	426	10	16
ENV	YDTEVINWV	14128	18	28	AKAYDTEVINWVATH	13472	71	15	23
ENV	AEGTDRIIE	14129	17	27	IAVAEGTDRIIEVVQ	13473	927	02	3
ENV	VOREKRAVG	14130	17	27	RRVOREKRAVGIGA	13474	582	05	8
ENV	AEGTDRVIE	14131	15	23	IAVAEGTDRVIEVVQ	13475	927	07	11
ENV	IEAQOHLK	14132	12	19	LRAIEAQOHLKLLTV	13476	642	08	13
ENV	LKCNDDKFN	14133	12	19	FAILKCNDDKFNFTG	13477	269	05	8
GAG	ANPDKTIL	14134	45	70	VQANPDKTILKAL	13478	347	27	42
GAG	FYKTLRAEQ	14135	28	44	VDRFYKTLRAEQASQ	13479	321	19	30
GAG	APGQMKRPR	14136	27	42	GPIAPGQMKRPRGSD	13480	242	19	30
GAG	FFKTLRAEQ	14137	27	42	VDRFFKTLRAEQATQ	13481	321	26	41
GAG	IWPSTIKGRP	14138	23	36	LGKIWPSTIKGRPGNF	13482	470	22	34
GAG	LARNCRAPR	14139	20	32	EGHILARNCRAPRKKG	13483	431	19	30
GAG	IANKRAPR	14140	18	29	EGHIAKNCRAPRKKG	13484	431	10	16
GAG	ATQEVKNWM	14141	18	28	AEQATQEVKNWMTET	13485	330	14	22
GAG	ATQDVKNWM	14142	15	23	AEQATQDVKNWMTDT	13486	330	11	17
GAG	IARNCRAPR	14143	13	21	EGHIAKNCRAPRKKG	13487	431	13	20
GAG	IWPSTIKGRP	14144	13	20	LGKIWPSTIKGRPGNF	13488	470	13	20
GAG	ANPDKSIL	14145	11	17	VQANPDKSILRAL	13489	347	06	9
GAG	ASQEVKNWM	14146	11	17	AEQASQEVKNWMTET	13490	330	11	17
GAG	IWPSSKGRP	14147	10	16	LGKIWPSSKGRPGNF	13491	470	10	16
NEF	LIYSKKRQE	14148	18	28	LDGLIYSKKRQELD	13492	171	11	17
NEF	MARELHPEY	14149	11	17	EKLVPVDPREVEAN	13493	227	06	9
NEF	MGYELHPDK	14150	10	16	FHHMARELHPEYYKD	13494	316	04	6
POL	FIHNFKRKG	14151	60	94	FLWMGYELHPDKWTV	13495	416	60	94
POL	MNKEKKII	14152	58	91	MAVFIHNFKRKGIGV	13496	930	57	89
POL	IIGQVRDQA	14153	56	89	VESMNKELKKIIGQV	13497	903	45	70
POL	YHSNWRAMA	14154	44	69	LKKIIGQVRDQAEHL	13498	910	43	67
POL	MEKEGKISK	14155	39	61	HEKYIHSNWRAMASDF	13499	764	23	36
POL	YVRDSRDP	14156	36	56	CTEMEKEGKISKIGP	13500	225	22	34
POL	ANRET'LGK	14157	34	53	FRVYYRDSRDPWKG	13501	975	34	54
POL	IGGQLKEAL	14158	30	47	DGAANRET'LGKAGY	13502	635	28	44
POL	LDKDFRYT	14159	25	39	'TIKIGGQLKEALLDT	13503	99	17	27
POL	YVRDSRDP	14160	19	30	SVPLDKDFRYTAF	13504	306	17	27
POL	IIGQVRDQA	14161	14	22	FRVYYRDSRDPWKG	13505	975	13	21
POL	YHSNWRAMA	14162	13	20	LKKIIGQVRDQAEHL	13506	910	13	20
POL	ARRNR'RRW	14163	10	16	HEKYIHSNWRAMASDF	13507	764	06	9
REV	ARKNR'RRW	14164	39	61	TQARRNR'RRWRAR	13508	38	18	28
REV	LLKTVRLIK	14165	18	28	TQARKNR'RRWRAR	13509	38	13	20
REV	VSSEVHIPL	14166	10	16	DEELLKTVRLIKFLY	13510	9	04	6
VIF	VSEVHIPL	14167	27	42	HPRISSSEVHIPLGDA	13511	48	08	13
VIF	VSEVHIPL	14168	27	42	HPKVSSEVHIPLGEA	13512	48	11	17
VIF	VSEVHIPL	14169	11	17	HGVSSEVHIPLRRYST	13513	85	05	8

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VPR	LPSNTRGIRG	14170	01	50	IGILPSNTRGRGRRN	13514	82	01	2
VPR	LLEELKNEA	14171	17	27	TLELLFELKNEAVRH	13515	19	12	19
VPR	LLEELKSEA	14172	16	25	TLELLFELKSEAVRH	13516	19	15	23
VPU	AKVDYRIVI	14173	01	33	DLLAKVDYRIVIVAF	13517	3	01	2
VPU	AKVDYRLGV	14174	01	33	NFLAKVDYRLGVGAL	13518	3	01	2
VPU	ILRQKKIDR	14175	15	23	YRKILRQKKIDRLID	13519	42	12	19

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
MRDNWRSEL	14120	GGDMRDNRSELYKY	13464								
LTVOAROLL	14121	SITLTVOAROLLSCI	13465								
IEAQQHLLQ	14122	LRAIEAQQHLLQLTV	13466								
IGDIROAH	14123	TGEIGDIROAHGNI	13467								
VEREKRAVG	14124	RRVVEREKRAVGIGA	13468								
MVEQMIEDI	14125	KNNMVEQMIEDISL	13469								
AWDDLRLSC	14126	LALAWDDLRLSLCLS	13470								
LETTISFN	14127	GGDLLETTISFNCRG	13471								
YDTEVINWV	14128	AKAYDTEVINWVATH	13472								
AEQTDRIE	14129	IAVAEGTDRIEIVVQ	13473								
VQREKRAVG	14130	RRVQREKRAVGIGA	13474								
AEQTDRIE	14131	IAVAEGTDRIEIVVQ	13475								
IEAQQHLLK	14132	LRAIEAQQHLLKLTV	13476								
LKCNCKFN	14133	FAILKCNCKFNKGTG	13477								
ANPCKTIL	14134	VQANPCKTILKAL	13478								
FYKTLRAEQ	14135	VDRFYKTLRAEQASQ	13479	0.0031							
APGQMRPR	14136	GPIAPGQMRPRGSD	13480	0.0049							
IFPSHKGRP	14137	VDRFFKTLRAEQATQ	13481	-0.0017							
LARNCRAPR	14138	EGHILARNCRAPRKG	13483								
IAKNCRAPR	14140	EGHIAKNCRAPRKG	13484								
ATQEVKNWM	14141	AEQATQEVKNWMTET	13485								
ATQDVKNWM	14142	AEQATQDVKNWMTDT	13486								
IARNCRAPR	14143	EGHIAKNCRAPRKG	13487								
IWPSNKGPR	14144	LGKIWPSNKGPRGNF	13488								
ANPCKSIL	14145	VQANPCKSILRAL	13489								
ASQEVKNWM	14146	AEQASQEVKNWMTET	13490								
IWPSKGRP	14147	LGKIWPSKGRPGNF	13491								
LIYSKKROE	14148	LDGLIYSKKROEILD	13492								
VPVDPREVE	14149	FKLVPVDPREVEEAN	13493								
MARELIPEY	14150	FHIMARELIPEYYKD	13494								
MGYELIIPDK	14151	FLWMGYELIIPDKWTV	13495								
FIHFKRKG	14152	MAVFIHFKRKGIG	13496	-0.0017							
MNKLKII	14153	VESMNKELKIIGQV	13497	0.0470							
IGQVRDQA	14154	LKKIIGQVRDQAEHL	13498								
YHNNWRAMA	14155	HEKYHNNWRAMASDF	13499								
MEKEGKISK	14156	CTEMEKEGKISKIGP	13500								
YYRDSRDPI	14157	FRVYYRDSRDPIWKG	13501								
ANRETKLKG	14158	DGAANRETKLKGAGY	13502								
IGQLKEAL	14159	TKIGQLKEALLDT	13503								
LKDPRKYT	14160	SVPLDKDPRKYTAFT	13504								
YYRDSRDPI	14161	FRVYYRDSRDPIWKG	13505								
IGQVREQA	14162	LKKIIGQVREQAEHL	13506								
YHNNWRAMA	14163	HEKYHNNWRAMASDF	13507								
ARRNRRRW	14164	TQARKNRRRRWRAR	13508								
ARKNRRRW	14165	TQARKNRRRRWRAR	13509								
LLKTVRLIK	14166	DEELKTVRLIKFLY	13510								
ISSEVHIPL	14167	IPRISSEVHIPLGDA	13511								
VSSEVHIPL	14168	HPKVSSEVHIPLGEA	13512								

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
MRDNWRSEL	14120	GGDMRDNRWSELYKY	13464					
LTVQARQLL	14121	SITLTVQARQLLSGI	13465					
IEAQHILLO	14122	LRAIEAQHILLQLTV	13466					
IGDIRQAH	14123	TGEIHGDIRQAHGNI	13467					
VEREKRAVG	14124	RRVVEREKRAVGIGA	13468					
MVEQMHHDI	14125	KNNMVEQMHHEDISL	13469					
AWDDLRSLC	14126	LALAWDDLRSLCLFS	13470					
LEITTHSFN	14127	GGDLEITTHSFNCRG	13471					
YDTEVINWV	14128	AKAYDTEVINWVATH	13472					
AEGTDRHIE	14129	IJVAEGTDRIIEVVQ	13473					
VQREKRAVG	14130	RRVVQREKRAVGIGA	13474					
AEGTDRVIE	14131	IJVAEGTDRVIEVVQ	13475					
IEAQHILK	14132	LRAIEAQHILLKLTV	13476					
LKNDKKFN	14133	FAILKNDKKFNGTG	13477					
ANPDKTIL	14134	VQNPDPCKTILKAL	13478					
FYKTLRAEQ	14135	VDRFYKTLRAEQASQ	13479					
APGQMRPR	14136	GPIAPGQMRPRGSD	13480					
FFKTLRAEQ	14137	VDRFFKTLRAEQATQ	13481					
IP'PSHKGRP	14138	LGKIWP'SHKGRPGNF	13482					
LARNCRAPR	14139	EGHILARNCRAPRKKG	13483					
IAKNCRAPR	14140	EGHIAKNCRAPRKKG	13484					
ATQEVKNWM	14141	AEQATQEVKNWMTET	13485					
ATQDVKNWM	14142	AEQATQDVKNWMTDT	13486					
IARNCRAPR	14143	EGHIARNCRAPRKKG	13487					
IWPSNKGPR	14144	LGKIWP'SNKGPRGNF	13488					
ANPDKSIL	14145	VQNPDPCKSILRAL	13489					
ASQEVKNWM	14146	AEQASQEVKNWMTET	13490					
IWPSKGRPR	14147	LGKIWP'SKGRPGNF	13491					
LIYSKKRQE	14148	LDGLYSKKRQEILD	13492					
VPVDPREVE	14149	FKLVVPDPREVEEAN	13493					
MARELIPEY	14150	FHHIMARELIPEYYKD	13494					
MGYELHPDK	14151	FLWMGYELHPDKWTY	13495					
FIHNFKRKG	14152	MAVFIHNFKRKGIG	13496					
MNKLKKH	14153	VESMNKLKKIIGQV	13497					
IGQVRDQA	14154	LKKIIGQVRDQAEHL	13498					
YHSNWRAMA	14155	HEKYHSNWRAMASDF	13499					
MEKEGKISK	14156	CTEMEKEGKISKIGP	13500					
YYRDSRDPH	14157	FRVYYRDSRDPHWKG	13501					
ANRETKLGK	14158	DGAANRETKLGKAGY	13502					
IGGOLKEAL	14159	TIKIGGOLKEALLDT	13503					
LDKDFRKYT	14160	SVPLDKDFRKYTFT	13504					
YYRDSRDPH	14161	FRVYYRDSRDPHWKG	13505					
IGQVREQA	14162	LKKIIGQVREQAEHL	13506					
YHNNWRAMA	14163	HEKYHNNWRAMASDF	13507					
ARNRRRRRW	14164	TRQARNRRRRRWRRAR	13508					
ARKNRRRRRW	14165	TRQARKNRRRRRWRRAR	13509					
LLKTVRLIK	14166	DEELLKTVRLIKFLY	13510					
ISSEVHIPL	14167	HPRISSEVHIPLGDA	13511					
VSEVHIPL	14168	HPKVSEVHIPLGEA	13512					
VSIEWRLRR	14169	GHGVSIIEWRLRRYST	13513					

0.0048

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2w81	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VSIEWRLRR	14169	GHGVSIEWRLRRYST	13513								
LPSNTRGRG	14170	IGIUPSNTRGRGRN	13514								
LLEELKNEA	14171	TLELEELKNEAVRII	13515								
LLEELKSEA	14172	TLELEELKSEAVRII	13516								
AKVDYRIVI	14173	DLLAKVDYRIVIVAF	13517								
AKVDYRLGV	14174	NFLAKVDYRLGVGAL	13518								
ILRQRKIDR	14175	YRKILRQRKIDRLID	13519	0.0024	0.0740	0.0410	13.0000	-0.0055		0.1500	

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LPSNTRGRG	14170	IGILPSNTRGRGRN	13514					
LLEELKNEA	14171	TLELLEELKNEAVRH	13515					
LLEELKSEA	14172	TLELLEELKSEAVRH	13516					
AKVDYRIVI	14173	DLLAKVDYRIVIVAF	13517					
AKVDYRLGV	14174	NFLAKVDYRLGVGAL	13518					
ILRQKIDR	14175	YRKILRQRKIDRLID	13519	0.0016	-0.0014	0.0270		

--TABLE III

MOTIFS	POSITION								
	1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4 preferred deleterious	FMYLIVW	M	T		I	VSTCPALIM	MH R		MH WDE
DR1 preferred deleterious	MFLIVWY			PAMQ		VMATSPLIC	M		AVM
DR7 preferred deleterious	MFLIVWY	M C	W C	A G		IVMSACTPL	M GRD		IV G
DR Supermotif	MFLIVWY					VMSTACPLI			
DR3 MOTIFS	1° anchor 1	2	3		1° anchor 4	5	1° anchor 6		
motif a preferred	LIVMFY				D				
motif b preferred	LIVMFAY				DNQEST		KRH		

Italicized residues indicate less preferred or "tolerated" residues.--

Table XXIII: Immunogenicity of HIV peptides

	Peptide	Seq ID	Sequence	Protein	Immunogenicity	
					patients	transgenic
A2 Supermotif	1261.04	14176	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	14177	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	14178	VLAEAMSQV	hiv gag 386	6/19	3/3
	1261.16	14179	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	14180	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	14181	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	14182	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	14183	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	14184	AIIRILQQL	HIV vpr 59	5/9	0/6
	1261.09	14185	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	14186	RILQQLLFI	HIV vpr 62	6/20	2/6
	1261.05	14187	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	14188	MTNNPPIPV	HIV gag 271	2/17	4/6
	1261.17	14189	KMIGGIGGFI	HIV pol 132	2/7	0/6
	941.03	14190	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	14191	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	14192	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	14193	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	14194	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	14195	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	14196	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	14197	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	14198	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	14199	QVPLRPMTYK	HIV nef 100	0/6	6/10
	1273.07	14200	TTLFCASDAK	HIV env 61	3/6	
	1273.09	14201	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	14202	TVYYGVVPVWK	HIV env 48		28/33
DR Supermotif	1069.47	14203	VTVYYGVVPVWK	HIV env 47	6/6	
	27	14204	KRWILGLNKIVRMY	HIV gag 298	3/13	
	27	14205	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27	14206	WEFVNTPLVKLWYQ	HIV pol 596	2/13	
	27	14207	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280	14208	KVYLAWVPAHKGIGG	HIV pol 712	3/13	
	27	14209	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27	14210	QGQMVHQAI SPRTL N	HIV gag 171	4/13	
	27	14211	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27	14212	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27	14213	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27	14214	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays			Radiolabeled peptide		
Species	Antigen	Allele	Cell line	Source	Seq ID Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	14215 YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	14216 FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	14217 FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	14218 FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	14219 FLPSDYFPSV
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	14220 FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	14221 KVFPYALINK
	A11		BVR	non-natural (A3CON1)	14222 KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	14223 AYIDNKNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	14224 KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	14225 KVFPYALINK
	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	14226 STLPETYVVR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	14227 FTQAGYPAL
	B7	B*0702	GM3107	A2 signal seq. 5-13 (L7->Y)	14228 APRTLVYLL
	B8	B*0801	Steinlin	HIVgp 586-593 Y1->F, Q5->Y	14229 FLKDYQLL
	B27	B*2705	LG2	R 60s	14230 FRYNGLIHR
	B35	B*3501	CIR, BVR	non-natural (B35CON2)	14231 FPFKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	14232 FPFKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	14233 FPFKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	14234 AEMGKYSFY
	B51		KAS116	non-natural (B35CON2)	14235 FPFKYAAAF
	B53	B*5301	AMAI	non-natural (B35CON2)	14236 FPFKYAAAF
	B54	B*5401	K13	non-natural (B35CON2)	14237 FPFKYAAAF
	Cw4	Cw*0401	CIR	non-natural (C4CON1)	14238 QYDDAVYKL
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	14239 YRHGGGNVL
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	14240 YRHGGGNVL
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	14241 SGPSNTYPEI
	K ^b		EL4	VSV NP 52-59	14242 RGYVFGGL
	D ^d		P815	HIV-IIIIB ENV G4->Y	14243 RGPYRAFVTI
	K ^d		P815	non-natural (KdCON1)	14244 KFNPMKTYI
	L ^d		P815	HBVs 28-39	14245 IPQSLDSYWTSI

B. Class II binding assays

Radiolabeled peptide					
Species	Antigen	Allele	Cell line	Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAATAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEAR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	DQA1*0301/DQB1*0301	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA ^d		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA ^k		CH-12	HEL 46-61	YNTDGGSTDYGILQNSR
	IA ^s		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA ^u		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKKAIYEKKK

TABLE XXVII
in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	Protei n	1st Position	Seq ID	sequence	Conservation (%)		A2-supertype binding capacity (IC50 nM)						alleles	
						total	B	A*0201	A*0202	A*020	A*0206	A*6802	bound		
1261.14	10	NEF	221	14273	LTFGWCFKLV	55	74	294.1	48.9	185.2	57.8	6.2	5		
1261.04	9	NEF	221	14274	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	5.6	4		
1261.06	9	POL	316	14275	YTAFTIPSI	58	68	26.3	6.1	9.1	7	16.7	5		
1261.15	10	POL	774	14276	MASDFNLPPV	39	68	62.5	22.6	55.6	33.6	18.2	5		
1069.32	9	GAG	386	14277	VLAEMSQV	52	74	66.6	82.7	15.2	115.6	363.6	5		
1261.16	10	POL	182	14278	CTLNFPISPI	94	100	147	23.9	30.3	8.4	100	5		
1261.02	9	ENV	651	14279	LLQLTVWGI	53	63	9.8	21.5	43.5	24.7	645.2	4		
1261.13	9	POL	448	14280	KLVGKLNWA	95	95	59.5	12.6	5.9	39.8	3076.9	4		
1211.04	9	ENV	134	14281	KLTPLCVTL	81	95	102	126.5	66.7	185	20000	4		
1261.08	9	POL	220	14282	ALVEICTEM	23	79	217.3	187	140.8	264.3	2857.1	4		
1261.11	9	VPR	59	14283	AIIRILQQL	61	74	333.3	22.6	41.7	38.5	547.9	4		
1261.09	9	POL	163	14284	LVGPTPVNI	84	100	454.5	153.6	19.2	2846.2	67.8	4		
1261.12	9	VPR	62	14285	RILQQLLFI	56	74	19.2	1535.7	125	37	1818.2	3		
1261.05	9	POL	183	14286	TLNFPISPI	97	100	75.7	1482.8	1.1	1947.4	57.1	3		
1261.03	9	GAG	271	14287	MTNNPIIPV	31	89	166.6	7166.7	33.3	1608.7	12.1	3		
1261.17	10	POL	132	14288	KMIGGIGGFI	97	95	172.4	54.4	4.8	770.8	3333.3	3		
941.03	9	POL	498	14289	ILKEPVHGV	64	79	192.3	2388.9	6.7	37000	363.6	3		
1260.10	9	POL	772	14290	RAMASDFNL	64	79	217.3	116.2	25000	52.1	3076.9	3		
1261.07	9	POL	879	14291	KAACWWAGI	49	79	277.7	1075	83.3	160.9	2666.7	3		
1211.09	10	ENV	814	14292	SLNATDIAV	22	68	9.8	1303	238.1	28.5	5479.4	3		
1211.05	9	ENV	608	14293	FLGAAGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7	2		
25.0053	9	VPR	66	14294	QLLIHFIRI	69	89	94.3	21500	25000	1608.7	476.2	2		
25.0139	10	GAG	270	14295	WMTNNPIIPV	31	89	98	3071.4	16.9	18500	2222.2	2		
1069.33	10	POL	993	14296	LLWKGEGAVV	95	100	111.1	632.4	25	770.8	3636.4	2		
25.0142	10	NEF	219	14297	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6	2		
1069.34	9	POL	993	14298	LLWKGEGAV	97	100	172.4	10750	21.7	1608.7	2666.7	2		
25.0161	10	POL	452	14299	KLNWASQIYA	42	84	217.3	3909.1	400	6166.7	3076.9	2		
1211.082	9	GAG	79	14300	SLYNTVATL	34	58	277.7	3583.3	50	37000	100000	2		
25.0037	9	GAG	486	14301	FLQSRPEPT	44	68	454.5	10750	32.3	18500	3076.9	2		
25.0046	9	POL	91	14302	TLWQRPLVT	61	68	270.2	21500	2500	18500	2857.1	1		

TABLE XXVIII

in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	Seq ID	sequence	Conservation (%)		A3-supertype binding capacity (IC50 nM)					alleles bound
						total	B	A*0301	A*1101	A*3101	A*3301	A*6801	
1273.01	9	GAG	163	14303	MVHQAI SPR	42	58	61.1	89.6	18.0	13.8	9.5	5
1193.0200	9	POL	572	14304	IVIWGKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5
1193.03	9	POL	931	14305	AVFIHNF KR	97	100	64.7	3.3	5.1	107.4	4.2	5
1193.01	9	POL	724	14306	YLA WVP AHK	34	95	142.9	105.3	327.3	33.0	2.0	5
1211.32	10	POL	971	14307	KIQNRVYYR	81	95	343.8	28.6	2.7	341.2	210.5	5
1069.49	10	POL	929	14308	QMAVFIHFK	94	100	9.2	8.5	268.7	432.8	400.0	4
1273.03	10	GAG	162	14309	QMVHQAI SPR	42	58	42.3	6000.0	243.2	290.0	186.0	4
1193.09	9	POL	353	14310	MTKILEPFR	67	84	13750.0	375.0	81.8	69.0	25.8	4
966.01	9	POL	347	14311	AIFQSSMTK	56	79	10.0	10.0	12000.0	96666.7	242.4	3
940.03	10	NEF	100	14312	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	133.3	3
1069.43	10	ENV	48	14313	TVYYGVVPVWK	64	95	11.0	3.5	1636.4	10357.1	14.5	3
1069.48	10	POL	931	14314	AVFIHNF KRK	91	100	114.6	20.7	1125.0	5000.0	307.7	3
1273.05	9	POL	99	14315	TIKIGGQLK	27	63	40.7	181.8	18000.0	36250.0	72.7	3
1273.06	9	ENV	64	14316	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3
1273.07	10	ENV	61	14317	TTLFCASDAK	78	84	119.6	27.3	9473.7	14500.0	140.4	3
1273.04	9	ENV	878	14318	RIVELLGRR	34	89	200.0	600.0	138.5	13809.5	444.4	3
1273.09	10	POL	98	14319	VTIKIGGQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3
1273.02	9	POL	246	14320	NTPVFAIKK	58	94.7	333.3	100.0	30000.0	48333.3	4.7	3
1150.14	9	POL	930	14321	MAVFIHFK	94	100	647.1	20.0	375.0	517.9	2.5	3
1273.08	9	VIF	7	14322	VMIVWQVDR	69	95	3235.3	272.7	3.8	5.3	2424.2	3
1069.47	11	ENV	47	14323	VTVYYGVVPVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3
1069.42	11	POL	722	14324	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3
1069.44	9	POL	855	14325	KLGRWVPVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3

TABLE XXIX

peptide	AA	protein	1st Position	Seq ID	sequence	Conservation (%)		B7-supertype binding capacity (IC50 nM)					bound
						total	B	B*0702	B*3501	B*5101	B*5301	B*5401	
I146.01	9	NIEF	94	14326	FPVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5
I296.01	9	ENV	259	14327	IPIHYCAPA	56	42	423	343	153	-	3.7	4
I5.0268	10	GAG	545	14328	YPLASLRSLF	15	32	392.9	480.0	39.3	150.0	714.3	4
I261.01	9	POL	186	14329	FPISPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3
I296.02	9	ENV	250	14330	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3
I296.03	11	POL	893	14331	IPYNPQSQGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3
29.0028	8	REV	75	14332	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3
I292.13	9	GAG	237	14333	HPVHAGPIA	30	74	50.0	11.6	13750.0	4428.6	4.3	3

Table XXX: A1-motif peptides

Peptide	Seq ID	Sequence	Protein	Conservancy		
				Total	Clade B	IC50 nM
1.0431	14334	EVNIVTDSQY	HIV pol 1187	83	93	472
1.0014	14335	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	14336	IYQYMDDL	HIV pol 359	78	87	391
1069.27	14337	VIYQYMDDL	HIV pol 358	78	87	446
1069.26	14338	VTVLVDVGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Seq ID	Sequence	Protein	Conservancy		
				Total	Clade B	IC50 nM
25.0113	14339	IWGCSGKLI	HIV env 69	69	91	444
25.0127	14340	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	14341	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	14342	PYNEWTLEL	HIV vpr 56	56	71	86
25.0123	14343	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	14344	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	14345	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	14346	TYQIYQPPF	HLVpol 1033	78	93	67
25.0115	14347	VWKEATTTL	HIV env 47	47	85	400
25.0218	14348	VWKEATTTLF	HIV env 47	47	85	44
25.0219	14349	YWQATWIPEW	HIV pol 96	96	93	182

Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	SEQ ID	Sequence	Protein	Conservancy		Immunogenicity	
				Total	Clade B	XRN	patients transgenic
1261.14	14350	LTFGWCFKLV	HIV nef 221	55	74	5	0/1 0/6
1261.04	14351	LTFGWCFKL	HIV nef 221	61	74	4	4/12 3/3
1261.06	14352	YTAFTIPSI	HIV pol 316	58	68	5	0/1 0/6
1261.15	14353	MASDFNLPPV	HIV pol 774	39	68	5	1/15 2/6
1069.32	14354	VLA EAM SQV	HIV gag 386	52	74	5	6/19 3/3
1261.16	14355	CTLNFPISPI	HIV pol 182	94	100	5	0/1 1/6
1261.02	14356	LLQLTVWGI	HIV env 651	53	63	4	2/8 1/6
1261.13	14357	KLVGKLNWA	HIV pol 448	95	95	4	3/15 3/3
1211.04	14358	KLTPLCVTL	HIV env 134	85	95	4	2/12 2/6
1261.08	14359	ALVEICTEM	HIV pol 220	23	79	4	0/2 1/6
1261.11	14360	AIIRILQQL	HIV vpr 59	61	74	4	5/9 0/6
1261.09	14361	LVGPTPVNI	HIV pol 163	84	100	4	1/9 1/6
1261.12	14362	RILQQLLFI	HIV vpr 62	56	74	3	6/20 2/6
1261.05	14363	TLNFPISPI	HIV pol 183	97	100	3	1/7 0/6
1261.03	14364	MTNNPIPIV	HIV gag 271	31	89	3	2/17 4/6
1261.17	14365	KMIGGIGGFI	HIV pol 132	97	95	3	2/7 0/6
941.03	14366	ILKEPVHGV	HIV pol 498	64	79	3	8/19 3/6
1261.10	14367	RAMASDFNL	HIV pol 772	64	79	3	2/9 0/6
1261.07	14368	KAACWWAGI	HIV pol 879	49	79	3	1/8 0/6
1211.09	14369	SLLNATDIAV	HIV env 814	22	68	3	

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

Peptide	SEQ ID	Sequence	Protein	Conservancy		Immunogenicity	
				Total	Clade B	XRN	transgenic patients
1211.32	14370	KIQNFRVYYR	HIV pol 971	81	95	5	4/6
1193.02	14371	IVIWGKTPK	HIV pol 572	75	79	5	0/6
1193.03	14372	AVFIHNFKR	HIV pol 931	97	100	5	3/6
1069.49	14373	QMAVFIHNFK	HIV pol 929	94	100	4	3/6
1150.14	14374	MAVFIHNFK	HIV pol 930	94	100	3	6/6
1069.48	14375	AVFIHNFKRK	HIV pol 931	91	100	3	0/6
1273.01	14376	MVHQAI SPR	HIV gag 163	42	58	5	0/6
1273.03	14377	QMVHQAI SPR	HIV gag 162	42	58	4	0/6
1193.01	14378	YLAWVPAHK	HIV pol 724	34	95	5	0/6
1069.42	14379	KVYLAWVPAHK	HIV pol 722	32	89	3	6/6
1193.09	14380	MTKILEPFR	HIV pol 353	67	84	4	0/8
966.01	14381	AIFQSSMTK	HIV pol 347	56	79	3	5/6
940.03	14382	QVPLRPMTYK	HIV nef 100	72	79	3	0/6
1069.44	14383	KLGRWPVK	HIV pol 855	78	68	3	
1273.02	14384	NTPVFAIKK	HIV pol 246	58	95	3	0/6
1273.08	14385	VMIVWQVDR	HIV vif 7	69	95	3	0/6
1273.04	14386	RIVELLGRR	HIV env 878	34	89	3	
1273.07	14387	TTLFCASDAK	HIV env 61	78	84	3	3/6
1273.06	14388	TLFCASDAK	HIV env 62	81	84	3	0/6
1273.09	14389	VTIKIGGQLK	HIV pol 98	27	63	3	6/6
1273.05	14390	TIKIGGQLK	HIV pol 99	27	63	3	0/6
1069.43	14391	TVYVGVPVWK	HIV env 48	64	95	3	28/33
1069.47	14392	VTVYVGVPVWK	HIV env 47	64	94	3	6/6

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	SEQ ID	Sequence	Protein	Binding capacity (IC50 nM)												DR Alleles	
				DR1	DR2w281	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53	bound
27.0313	14393	KRWIIILGLNKIVRMY	HIV gag 298	4.2	5.1	24	188	633	404	54	124	0.36	379	49	58		12
27.0354	14394	WEFVNITPLVLKLYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	90	15	350	39		10
27.0377	14395	QKQITKIQNFRVYYR	HIV pol 956	2.9	3.4	80	-	357	49	53	124	25	25	75	577		11
1280.03	14396	KVYLAWVPAAHKGIGG	HIV pol 712	8.3	25	24	-	156	165	71	12598	2500	179	196	250		9
27.0311	14397	GEYKRWIIILGLNKI	HIV gag 294	82	138	225	-	1667	380	213	1656	98	192	63	536		9
27.0361	14398	EKVYLAWVPAAHKGIG	HIV pol 711	3.6	21	4.9	3226	9.3	27	37	6478	3500	18	31	144		9
27.0297	14399	QHLLQLTVWGKQLQ	HIV env 729	6.1	21	690	-	1316	345	2128	1064	350	44	907	375		8
27.0304	14400	QQQMVHQVAISPTLN	HIV gag 171	72	65	13	17647	60	400	-	-	412	455	7313	117		8
27.0344	14401	SPAIFQSSMTKILEP	HIV pol 335	357	217	667	-	3571	109	741	-	13	68	3267	33		8
F091.15	14402	IKQFINMWQEVGKAMY	HIV env 566	128	217	206	-	417	271	4878	-	1000	-	350	5769	104	8
27.0341	14403	FRKYTAFTIPSINNE	HIV pol 303	185	70	4167	-	294	136	1818	-	-	30	803	39		7
27.0364	14404	HSNWWRAMASDFNLPP	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	1960	872		7
27.0373	14405	KTAVQMAVFIHNFKR	HIV pol 915	161	650	690	-	909	452	182	18625	125	1786	1441	2586		7

A dash indicates IC50>20μM

Table XXXVI: DR3 binding peptides

Peptide	Seq ID	Sequence	Protein	DR3
35.0135	14406	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	14407	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	14408	EVNIVTDSQYALGII	HIV pol 674	732
35.0125	14409	AETFYVDGAANRETK	HIV pol 619	769
35.0133	14410	GAVVIQDNSDIKVVP	HIV pol 989	1000

TABLE XXXVII

Immunogenicity of HIV-derived DR-supermotif peptides

Peptide	Seq ID	Sequence	Protein	Conservation (%)		DR Alleles bound	Patient Immunogenicity
				total	clad B		
27.0313	14111	KRWILGLNKIVRMY	HIV gag 298	85 [89] ¹	94 [95]	12	3/13
27.0311	14112	GEIYKRWIILGLNKI	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	14113	WEFVNTPL VKLWYQ	HIV pol 596	79 [89]	84 [95]	10	3/13
27.0377	14114	QKQITKIQNFRVYYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	14115	KVYLAWVPAHKGIGG	HIV pol 712	32 [34]	89 [95]	9	3/13
27.0361	14116	EKVYLAWVPAHKGIG	HIV pol 711	32 [34]	94 [95]	9	1/13
27.0304	14117	QQQMVHQAI SPRTLN	HIV gag 171	41 [42]	52 [58]	8	4/13
27.0344	14118	SPAIFQSSMTKILEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	14119	FRKYTAFTIPSINNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	14120	HSNWRAMASDFNLPP	HIV pol 758	48 [67]	68 [79]	7	3/13
27.0373	14121	KTAVQMAVFIHNFKR	HIV pol 915	87 [95]	94 [100]	7	4/13

1: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Seq ID	Sequence
HLA-A2	1069.32	HIV gag 386	14122	VLAEAMSQV
"	1261.03	HIV gag 271	14123	MTNNPPIPV
"	1261.15	HIV pol 774	14124	MASDFNLPPV
"	1261.13	HIV pol 448	14125	KLVGKLNWA
"	1261.09	HIV pol 163	14126	LVGPTPVNI
"	941.03	HIV pol 498	14127	ILKEPVHGV
"	1261.07	HIV pol 879	14128	KAACWWAG
"	1261.17	HIV pol 132	14129	KMIGGIGGFI
"	1261.10	HIV pol 772	14130	RAMASDFNL
"	1261.05	HIV pol 183	14131	TLNFPISPI
"	1211.04	HIV env 134	14132	KLTPLCVTL
"	1261.02	HIV env 651	14133	LLQLTVWGI
"	1211.09	HIV env 163	14134	SLLNATDIAV
"	1261.04	HIV nef 221	14135	LTFGWCFKL
"	1261.11	HIV vpr 59	14136	AIIRILQQL
"	1261.12	HIV vpr 62	14137	RILQQLFI
HLA-A3	1069.49	HIV pol 929	14138	QMAVFIHNFF
"	1069.42	HIV pol 722	14139	KVYLAWVPA
"	1211.32	HIV pol 971	14140	KIQNFRVYYR
"	1193.09	HIV pol 353	14141	MTKILEPFR
"	966.01	HIV pol 347	14142	AIFQSSMTK
"	1273.09	HIV pol 98	14143	VTIKIGGQLK
"	1273.07	HIV env 61	14144	TTLFCASDAK
"	1069.47	HIV env 47	14145	VTVYYGVPVV
"	940.03	HIV nef 100	14146	QVPLRPMTYK
"	1273.08	HIV vif 7	14147	VMIVWQVDR
"	1273.03	HIV gag 162	14148	QMVHQAISPF
HLA-B7	15.0268	HIV gag 545	14149	YPLASLRSLF
"	1292.13	HIV gag 237	14150	HPVHAGPIA
"	1261.01	HIV pol 186	14151	FPISPIETV
"	1296.03	HIV pol 893	14152	IPYNPQSQGV
"	1296.01	HIV env 259	14153	IPIHYCAPA
"	1296.02	HIV env 250	14154	CPKVSFEPI
"	1146.01	HIV nef 94	14155	FPVRPQVPL
"	29.0028	HIV rev 75	14156	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	14157	EVNIVTDSQY
"	1.0014	HIV gag 317	14158	FRDYVDRFY
"	1069.27	HIV pol 368	14159	VIYQYMDDL
"	1069.26	HIV pol 295	14160	VTVLVDVGDA
HLA-A24	1069.60	HIV pol 533	14161	IYQEPFKNL
"	25.0123	HIV pol 244	14162	PYNTPVFAI
"	1069.59	HIV pol 530	14163	TYQIYQEPF
"	25.0219	HIV pol 597	14164	YWQATWIPEV
"	25.0113	HIV env 681	14165	IWGCSGKLI
"	1069.57	HIV env 671	14166	RYLKDQQLL
"	25.0115	HIV env 55	14167	VWKEATTTLF
"	25.0127	HIV vpr 46	14168	IYETYGDTW
"	25.0128	HIV vpr 14	14169	PYNEWTLEL

Table XXXIX: HTL Candidate Epitopes

Selection Criteria	Peptide	Seq ID	Sequence	Protein
DR	27.0313	14170	KRWIILGLNKIVRMY	HIV gag 298
	27.0354	14171	WEFVNTPLVLKLYQ	HIV pol 596
	27.0377	14172	QKQITKIQNFRVYYR	HIV pol 956
	1280.03	14173	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	14174	GEIYKRWIILGLNKI	HIV gag 294
	27.0361	14175	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	14176	QHLLQLTVWGIKQLQ	HIV env 729
	27.0304	14177	QGQMVHQAI SPRTL N	HIV gag 171
	27.0344	14178	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	14179	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	14180	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	14181	HSNWRAMASDFNLPP	HIV pol 758
	27.0373	14182	KTAVQMAVFIHNFKR	HIV pol 915
DR3	35.0135	14183	YRKILRQRKIDRLID	HIV vpu 31
	35.0131	14184	WAGIKQEF GIPY NPQ	HIV pol 874
	35.0127	14185	EVNIVTDSQYALGII	HIV pol 674
	35.0125	14186	AETFYVDGAANRETK	HIV pol 619
	35.0133	14187	GAVVIQD NSDIK VVP	HIV pol 989